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Pred. No. is the number of results predicted by chance to have a

Result No.	Score	Query Match	Length	DB	ID	Description
1	1146	100.0	1146	6	E13814	E13814 CDNA encod
2	1146	100.0	1335	9	AF003594	AF003594 Homo sapi
3	1146	100.0	1985	6	BC001271	BC001271 Homo sapi
4	1146	100.0	2016	6	AX336386	AX336386 Sequence
5	1146	100.0	2016	6	AX354335	AX354335 Sequence
6	1146	100.0	2016	6	HS062015	HS062015 Homo sapien
7	1146	100.0	2021	9	HS0161PT	HS0161PT Homo sapien
8	1146	100.0	2025	9	HSCYR81M	HSCYR81M Homo sapien
9	1146	100.0	2041	9	BC016952	BC016952 Homo sapi
10	1146	100.0	2045	9	BC009199	BC009199 Homo sapi
11	1144.4	99.9	2052	9	HSCYR61	Y11307 H.sapiens C
12	1142.8	99.7	1418	6	AX306704	AX306704 Sequence
13	1142.8	99.7	2270	6	AX035239	AX035239 Sequence
14	1142.8	99.7	2270	6	AX342093	AX342093 Sequence
15	1142.8	99.7	2270	6	AX342153	AX342153 Sequence
16	1142.8	99.7	2270	6	AX344156	AX344156 Sequence
17	1141.2	99.6	1887	9	AF031385	AF031385 Homo sapi
18	1075.6	93.9	1128	6	AY463811	AY463811 Sequence
19	907.2	79.2	1220	9	AF003114	AF003114 Homo sapi
20	896	78.2	1480	6	AX206702	AX206702 Sequence
21	896	78.2	2018	10	M05CYR61A	M32490 Mouse Cytrb1
22	894.4	78.0	1987	10	AF218568	AF218568 Rattus no
23	888	77.5	1871	10	AB011877	AB011877 Rattus no
24	663.4	53.7	1805	5	CHKCF	J04436 Chicken CEF
25	615.6	53.7	1860	9	AK096420	AK096420 Homo sapi
26	615.6	53.7	180574	9	AC092807	AC092807 Homo sapi
27	606.4	52.9	4468	9	AF307860	AF307860 Homo sapi
28	567.4	49.5	1743	5	AF320592	AF320592 Xenopus l
29	513	44.8	806	6	AX210560	AX210560 Sequence
30	505	44.1	1687	9	HSM804202	AL832891 Homo sapi
31	325.6	28.4	173461	2	AC142690	AC142690 Rattus no
32	302.4	26.4	304	9	HSA333210	Z50168 H.sapiens p
33	288.6	25.2	5196	10	MMCYR61G	X56790 Mouse growt
34	214	18.0	255	6	AX210743	AX210743 Sequence
35	205.8	18.0	2190	5	AF463517	AF463517 Gallus ga
36	205.8	18.0	2288	5	AJ298335	AJ298335 Gallus ga
37	204.4	17.8	2075	6	AR118837	AR118837 Sequence
38	204.4	17.8	2075	6	AR118835	AR118835 Sequence
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42	204.4	17.8	2075	6	132210	132210 Sequence 1
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44	204.4	17.8	2312	9	HSCYR7	XY8947 H.sapiens m
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REFERENCE
1 (bases 1 to 1146)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

Pred. No. is the number of results predicted by chance to have a

FILE	MONOCYTIC MATURATION DIFFERENTIATION FACTOR
PATENT	JP 1997234079-A 1 09-SEP-1997;
COMMENT	TOYOKO CO. LTD
OS	Homo sapiens (human)
PN	JP 1997234079-A/1
PD	09-SEP-1997
PF	04-MAR-1996 JP 1996075236
PI	OOI KIYOMOTO, SATSU TAKASHII, KIZUMOTO MASAMI, HARA HISANORI,
PI	SEKI TATSUYA,
PI	SHIMONISHI MANABU, NAGASAWA TETSUJI, SAKAI HARUMI, PI
SHIMIZU NORIHIRO,	
PI	HAGIYA MICHIO,
PC	C12N15/09,A61K38/00,A61K38/00,A61K38/00,A61K38/00,
PC	C07H21/04,
PC	C07K14/47,C07K14/52,C12N5/10,C12P21/02,(C12P21/02,C12R1:91);
CC	strandedness: Double;
CC	topology: Linear;
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OY	61 CTGGGCGCTCTCCACCTGCGCCGCTGCGTCGTCACCTGCGCCGCGCCGCGCCGCGCGCG 120
Db	61 CTGGGCGCTCTCCACCTGCGCCGCTGCGTCGTCACCTGCGCCGCGCCGCGCCGCGCGCG 120
OY	121 CCGGAGTCGGGCTGGTCCGGGACGCGTCGCGCTGCTGAAGGTCTGGCCCAAGCAGCTC 180
Db	121 CCGGAGTCGGGCTGGTCCGGGACGCGTCGCGCTGCTGAAGGTCTGGCCCAAGCAGCTC 180
OY	181 AACGAGGACTGCAGCAAAACGACGCCCTGCGACCAACCAAGGGGCTGGAATGCAACTTC 240
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OY	301 GAATTAACCTCCAGATCTACCAAAAGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 360
Db	301 GAATTAACCTCCAGATCTACCAAAAGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 360
OY	361 TGCACATGTATTGATGGCGCGTGGGCTGCAATCTCTGTGTGTCGCCAAGAACTATCTCTC 420
Db	361 TGCACATGTATTGATGGCGCGTGGGCTGCAATCTCTGTGTGTCGCCAAGAACTATCTCTC 420
OY	421 CCCAACTGGGCTGTCGCCAACCCTGGCTGGTCAAGATTACCGGGCAGGCTGGCAGAGGAG 480
Db	421 CCCAACTGGGCTGTCGCCAACCCTGGCTGGTCAAGATTACCGGGCAGGCTGGCAGAGGAG 480

Accession	Source	Organism	Accession	Source	Organism	
OY	481	TGGGCTGTGACGAGGATAGATATCAAGAACCCCATGAGACACGAGCGCTCTTGGC	540	OY	481	TGGGCTGTGACGAGGATAGATATCAAGAACCCCATGAGACACGAGCGCTCTTGGC
Db	481	TGGGCTGTGACGAGGATAGATATCAAGAACCCCATGAGACACGAGCGCTCTTGGC	540	OY	541	AAGGAGCTGCGATTTCGATGCTCCGAGGTGAGTTGACGAGAAACAATGAATGATTGCA
OY	541	AAGGAGCTGCGATTTCGATGCTCCGAGGTGAGTTGACGAGAAACAATGAATGATTGCA	600	Db	541	AAGGAGCTGCGATTTCGATGCTCCGAGGTGAGTTGACGAGAAACAATGAATGATTGCA
OY	601	GTGGAAGGAGCTGCTACTGACGAGCGCTCCCTTTTGGAAATGAGACCTCGCATCTTA	660	OY	601	GTGGAAGGAGCTGCTACTGACGAGCGCTCCCTTTTGGAAATGAGACCTCGCATCTTA
Db	601	GTGGAAGGAGCTGCTACTGACGAGCGCTCCCTTTTGGAAATGAGACCTCGCATCTTA	660	OY	661	TACAAACCTTTACAAAGCCCAACAATGATTTTTCACAAACACTTTCATGCTCCATGCTCA
OY	661	TACAAACCTTTACAAAGCCCAACAATGATTTTTCACAAACACTTTCATGCTCCATGCTCA	720	Db	661	TACAAACCTTTACAAAGCCCAACAATGATTTTTCACAAACACTTTCATGCTCCATGCTCA
OY	721	AAGACCTGTGACATGCTGATCTCCACACAGATTACCAATGACCAACCTGAGTGGCGCTT	780	OY	721	AAGACCTGTGACATGCTGATCTCCACACAGATTACCAATGACCAACCTGAGTGGCGCTT
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OY	781	GTGAAGAAACCCGAGATTGTGAGGTGGCGCTTGTGAGACGCCAGTGTCACGACGCTG	840	Db	781	GTGAAGAAACCCGAGATTGTGAGGTGGCGCTTGTGAGACGCCAGTGTCACGACGCTG
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OY	901	GCTGGATGTTTGAAGTGTGAAGAATAACCGGCGCCACAGTACGCTGCTGCTGAGACGCG	960	Db	901	GCTGGATGTTTGAAGTGTGAAGAATAACCGGCGCCACAGTACGCTGCTGCTGAGACGCG
OY	961	CGATGCTGCACGCGCCACGCTGACGACGAGACTGTGAAGATGCGGTTCCGCTGGGAAGATGG	1020	OY	961	CGATGCTGCACGCGCCACGCTGACGACGAGACTGTGAAGATGCGGTTCCGCTGGGAAGATGG
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DB      124 ATGAGCTCCGATCGCCAGGCGCTGCTTACTGCTCAACCTTCTCACTTGACCAAG 183
QY      61  CTGGCGCTTCACCTCCCGCTGCTGCCACTGCCCTTGAGAGGCCCAAGTGGCG 120
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DB      184 CTGGCGCTTCACCTCCCGCTGCTGCCACTGCCCTTGAGAGGCCCAAGTGGCG 243
QY      121 CCGGAGTGGGCGTGGTCCGGAGGCGTGGGGGCTGTAGAGTCTGCGCAACGACGCTC 180
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DB      244 CCGGAGTGGGCGTGGTCCGGAGGCGTGGGGGCTGTAGAGTCTGCGCAACGACGCTC 303
QY      181 AACGAGACTGACAGCAAAAGCAGCCCTGCGACCAACCAAGSGGCTGATGCAATTC 240
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DB      304 AACGAGACTGACAGCAAAAGCAGCCCTGCGACCAACCAAGSGGCTGATGCAATTC 363
QY      241 GCGCGCAGCTCACCGCTCTGAGGGATCTGCAGAGCTCAAGTAGAGGCGACACCTGT 300
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DB      364 GCGCGCAGCTCACCGCTCTGAGGGATCTGCAGAGCTCAAGTAGAGGCGACACCTGT 423
QY      301 GAATATTAATCCCAATCTACCAAAAGGGGAAGTTCCAGCCCACTGTAAACATCAG 360
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DB      424 GAATATTAATCCCAATCTACCAAAAGGGGAAGTTCCAGCCCACTGTAAACATCAG 483
QY      361 TGCACATGATATGATGGCGCGCTGGCTGCAATTCCTGTGTCCCAAGAACTATCTCTC 420
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DB      484 TGCACATGATATGATGGCGCGCTGGCTGCAATTCCTGTGTGTCCCAAGAACTATCTCTC 543
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DB      784 TACAACCTTTACAGAGCAAGAAATGATTGTTCAACCACTTATGATGCTCCAGTCTCA 843
QY      721 AAGACCTGTGAACTGTTATCTCCACAGAGATTACCAATGACAAACCTGAGTGGCGCCTT 780

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QY      841 AAAAAGGCAAGAAATGACAGACAGACAGAAATCCCGGACAGCAGATTTACTTAC 900
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DB      964 AAAAAGGCAAGAAATGACAGACAGACAGAAATCCCGGACAGCAGATTTACTTAC 1023
QY      901 GCTGATGTTTGAAGTGTGAAGAAATACCGGCGCAAGTACTGCGTTCTGCTGAGAGGC 960
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DB      1024 GCTGATGTTTGAAGTGTGAAGAAATACCGGCGCAAGTACTGCGTTCTGCTGAGAGGC 1083
QY      961 CGATGCTGACAGCCCGCAGCTGACAGACAGTGTGAAGATGGGTTCCCTCGGAAGATGG 1020
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DB      1084 CGATGCTGACAGCCCGCAGCTGACAGACAGTGTGAAGATGGGTTCCCTCGGAAGATGG 1143
QY      1021 GAGACATTTTCCAAAGACGTCATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
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DB      1144 GAGACATTTTCCAAAGACGTCATGATGATGATGATGATGATGATGATGATGATGATGATG 1203
QY      1081 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGAGCTGTTCATGACATTCACAAATTTAGG 1140
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DB      1204 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGAGCTGTTCATGACATTCACAAATTTAGG 1263
QY      1141 GACTAA 1146
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DB      1264 GACTAA 1269

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RESULT 3

BC001271

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

ORGANISM

SOURCE

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
 Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 DNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcdpaxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

Clone distribution: MGC clone distribution information can be found
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 Series: IRAX Plate: 4 Row: h Column: 9
 This clone was selected for full length sequencing because it
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FEATURES

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Best Local Similarity	100.0%;	Pred. No. 2.5e-235;		
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			Gaps	0;

QY	1	TTGAGCTCCCGCATTCGACAGGAGCGCTGCCTTACGTGACACCTTTCACATTGACAGG	60
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QY	661	TACAAACCTTTACAAAGGCCAGAAATGTATTGTCTTAAACAACTTATGTGCCAGTGTCTCA	720
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QY	721	AAGACGCTGGAACTGAGTATCTCCAGACGAGTTACCAATGACAAACCGTAGTGGCGCTT	780
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Db	1240	CATGCCAATGAAAGCAGCGTTCCCTTGTACAGGCTGTTCAATGACATTTCAACAAATTTAGG	1299
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LOCUS	AX336386	2016 bp	DNA	linear	PAT 09-JAN-2002
DEFINITION	Sequence 6895 from Patent WO0194629.				
ACCESSION	AX336386				
VERSION	AX336386.1	GI:18127105			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	1				
TITLE	Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Eriksen,G., Horigan,S., Soppet,D.R. and Weaver,Z.				
JOURNAL	Cancer gene determination and therapeutic screening using signature gene sets				
FEATURES	Patent: WO 0194629-A 6895 13-DEC-2001; Avalon Pharmaceuticals (US) location/Qualifiers				
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BASE COUNT	490 a 525 c 534 g 467 t				
ORIGIN					

Query Match	100.0%	Score 1146	DB 6	Length 2016
Best Local Similarity	100.0%	Pred. No. 2.5e-235		
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Db	270	CTGGCGCTCTCCACTGCCCCGCTGCTGCACATGCCCCGTGAGAGCGCCCAAGTGGCG	329	
QY	121	CCGGGATCGGGGCTGCGGAGAGCGTGTGGGGCTGTAAAGTCTCGGCAAGACACTC	180	
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 QY 541 AAGGAGCTGGGATTCGATGGCTCGAGGTGAGTTCAGAGAAACAAATGATGATTGCA 600
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 DB 1350 GACTAA 1355

RESULT 5
 AX354335
 LOCUS

AX354335

2016 bp

DNA

linear

PAT 06-FEB-2002

DEFINITION Sequence 1 from Patent WO0198359.
 ACCESSION AX354335
 VERSION AX354335.1 GI:18619194
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1
 AUTHORS Sampath,D., Zhang,Z. and Winneker,R.
 TITLE Cytr61 as a target for treatment and diagnosis of breast cancer
 JOURNAL Patent: WO 0198359-A 1 27-DEC-2001;
 AMERICAN HOME PRODUCTS CORPORATION (US)
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 1. 2016
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 BASE COUNT 490 a 525 c 534 g 467 t
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 Query Match 100.0%; Score 1146; DB 6; Length 2016;
 Best Local Similarity 100.0%; Pred. No. 2,5e-235;
 Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGAGCTCCGCATCGCCAGGCGCTGCGCTTATGCTCAACCTTCTCCACTTGACCAAG 60
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 QY 541 AAGGAGCTGGGATTCGATGGCTCGAGGTGAGTTCAGAGAAACAAATGATGATTGCA 600
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RESULT 6
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 LOCUS HS062015 2016 bp mRNA linear PRI 28-MAY-1997
 DEFINITION Homo sapiens Cyr61 mRNA, complete cds.
 ACCESSION U62015
 VERSION 062015.1 GI:2130526
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens.

REFERENCE
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 2016)
 Jay, P., Berge-Lefranc, J. L., Marsollier, C., Mejean, C., Tavlaux, S.
 and Beria, P.
 The human growth factor-inducible immediate early gene, CYR61, maps
 to chromosome 1p

TITLE
 JOURNAL Oncogene 14 (14), 1753-1757 (1997)
 MEDLINE 9728750
 PUBMED 9135077
 REFERENCE 2 (bases 1 to 2016)
 AUTHORS Jay, P.
 TITLE Direct Submission
 JOURNAL Submitted (25-JUN-1996) Philippe Jay, Centre de Recherches de
 Biochimie Macromoleculaire, CNRS/INS, Campus CNRS, 1919 route de
 Mende, Montpellier 34033, France
 Location/Qualifiers
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FEATURES
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BASE COUNT 490 a 525 c 534 g 467 t
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 Query Match 100.0%; Score 1146; DB 9; Length 2016;
 Best Local Similarity 100.0%; Pred. No. 2.5e-235;
 Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGAGCTCCGCAATGCAAGGAGGCGCTGCGCTTGTGATGATGATGATGATGATGATG 60
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Db 1350 GACTAA 1355
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DEFINITION H. sapiens mRNA for g1g1 protein.
ACCESSION Y12084
VERSION Y12084.1 GI:2181870
KEYWORDS g1g1 gene; G1g1 protein.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2021)
AUTHORS Albrecht, C., von Der Kammer, H., Mayhaus, M., Klaudiny, J.,
Schweizer, M. and Nitsch, R.M.
TITLE Immediate acetylcholine receptors induce the expression of the
JOURNAL immediate early growth regulatory gene CYR61
MEDLINE J. Biol. Chem. 275 (37), 28929-28936 (2000)
PUBMED 10852911
REFERENCE 2 (bases 1 to 2021)
AUTHORS von der Kammer, H.
TITLE Direct Submission
JOURNAL Submitted (01-APR-1997) H. von der Kammer, Zentrum fuer Molekulare
Neurobiologie Hamburg, Martinistr. 52, D-20246 Hamburg, FRG
FEATURES
source location/Qualifiers
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Query Match 100.0%; Score 1146; DB 9; Length 2021;
Best Local Similarity 100.0%; Pred. No. 2.5e-235;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 8
LOCUS HSCYR61M 2025 bp mRNA linear PRI 03-FEB-1998
DEFINITION Homo sapiens mRNA for hcyR61 protein.
ACCESSION 298053
VERSION 298053.1 GI:2832336
KEYWORDS hcyR61 protein.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Schuetz, N., Lechner, A., Groll, C., Koehle, J. and Jakob, F.
TITLE Regulation of hcyR61 by vitamin D, serum and cytokines in fetal
human osteoblasts
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2025)
AUTHORS Schuetz, N.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1997) Klinische Forschergruppe, Medizinsische
Poliklinik, Koentgenring 11, Weirzburg 97070, Germany
FEATURES
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Location/Qualifiers
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BASE COUNT 490 a 531 c 537 g 467 t

Query Match 100.0%; Score 1146; DB 9; Length 2025;
Best Local Similarity 100.0%; Pred. No. 2.5e-235;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS BC016952 2041 bp mRNA linear PRI 09-NOV-2001
DEFINITION Homo sapiens, clone MGC:21510 IMAGE:3886130, mRNA, complete cds.
ACCESSION BC016952
VERSION BC016952.1 GI:16877412
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2041)

AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (05-NOV-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabs-femail.nih.gov
 Tissue Procurement: DCTD/DRP/Gazdar
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) medepaxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

FEATURES
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BASE COUNT 509 a 529 c 535 g 468 t

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Query Match 100.0%; Score 1146; DB 9; Length 2041;
 Best Local Similarity 100.0%; Pred. No. 2.5e-235;
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RESULT 10
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 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eulhelia; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 2046)
 AUTHORS Strausberg, R.
 TITLE Direct Submission

JOURNAL

Submitted (06-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>

Contact: MGC help desk

Email: cgapds@mail.nih.gov

Tissue Procurement: ATCC/DC/DMP

CDNA Library Preparation: Rubin Laboratory

DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)

<http://www.systemsbio.org>

Contact: amadan@systemsbiology.org

Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia Greene, Mark Kettelman and Anuradha Madan

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAL Plate: 24 Row: f Column: 2
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 2130526.

FEATURES

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BASE COUNT 511 a 532 c 536 g 467 t
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Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 11

HSCYR61

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

HSCYR61
H. sapiens CYR61 mRNA.
Y11307.1 GI:2791897
cy61 gene; cy61 protein.
Homo sapiens.
Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 2052)
Martinerie/C., Viegas-Pequignot/E., Nguyen/V.C. and Perbal,B.
Chromosomal mapping and expression of the human CYR61 gene in tumor
cells from the nervous system
J. Clin. Pathol. Mol. Pathol. 50, 130-136 (1997)

REFERENCE 2 (bases 1 to 2052)
 AUTHORS Peral, B.
 TITLE Direct Submission
 JOURNAL Submitted (17-FEB-1997) B. Peral, Institut Curie, Centre
 Universitaire, Bat 110, 91405 Orsay Cedex, FRANCE
 COMMENT Related sequence M32490.
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 BASE COUNT 499 a 542 c 543 g 468 t
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 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1418)
 AUTHORS Lau, L.F., Yeung, C.Y., and Greenspan, J.A.
 TITLE Cyrl61 compositions and methods
 JOURNAL Patent: WO 0155210-A 3 02-AUG-2001;
 Munit Corporation (US)
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ACCESSION	AX035239				
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AUTHORS	Glennie,J., Hinman,B., Pilarsky,C. and Thierauch,K.H.				
TITLE	Human nucleic acid and protein sequences obtained from endothelial cells				
JOURNAL	Patent: WO 0053734-A 56 14-SEP-2000;				
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VERSION AX342093.1				
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE 1				
AUTHORS Siemielster G., Haberey M. and Thierunch K.H.				
TITLE Combinations and compositions which interfere with vegf/vegf and				
angiopoietin1, the receptor function and their use				
JOURNAL Patent: EP 1166798-A 56 02-JAN-2002.				

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ACCESSION AX342153
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Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1 Stenmister, G., Haberey, M. and Thierauch, K. H.
TITLES Combinations and compositions which interfere with vegf/vegf and
angiopoietin/tie receptor function and their use (11)
JOURNAL Patient: EP 1166799-A 56 02-JAN-2002;
SCHERING AKTIEGENESLSCHAFT (DE)
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Location/Qualifiers
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Best Local Similarity 99.8%; Pred. No. 1.2e-234;
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GenCore version 5.1.6
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SUMMARIES

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19	1141.2	99.6	1887	24	ABO88131	Human osteoblast d
20	1075.6	93.9	1128	17	AA112653	Connective tissue
21	1075.6	93.9	1128	24	AAAD9099	Human alternative
22	1073	93.6	1128	20	AAZ11720	Human CTGF-1 CDNA
23	896	78.2	1480	22	AAAD11220	Mouse cysteine-ric
24	896	78.2	2028	13	AAO26421	Gene for beta-IG-W
25	513	44.8	806	22	AAH81693	Human differential
26	426.6	37.2	493	24	ABO61145	Human colon cancer
27	372	35.5	372	15	AAO57417	CYR61 like protein
28	214	18.7	255	22	AAH81876	Rat differential t
29	204.4	17.8	2075	16	AAAT04226	Connective tissue
30	204.4	17.8	2075	18	AAAT45360	Human connective t
31	204.4	17.8	2075	18	AAAT51234	Connective tissue
32	204.4	17.8	2075	19	AAV38085	Human connective t
33	204.4	17.8	2075	20	AAAX61317	Human connective t
34	204.4	17.8	2075	21	AAAI12878	Human connective t
35	204.4	17.8	2075	21	AAAI1280	Human connective t
36	204.4	17.8	2075	22	AAAD11223	Human connective t
37	204.4	17.8	2075	22	AAFS9954	Human connective t
38	204.4	17.8	2075	22	AAAC87517	Human connective t
39	204.4	17.8	2075	25	ABK64553	Human benign prost
40	204.4	17.8	2312	22	AAH28213	Nucleotide sequenc
41	204.4	17.8	2312	22	AAH07914	Human shear stress
42	202.6	17.7	351	21	AAAH4347	Human secreted exp
43	200	17.5	2330	13	AAO26422	Gene for beta-IG-W
44	198.4	17.3	2267	18	AAI94700	Murine Fisp12 CDNA
45	198.4	17.3	2267	22	AAAD11222	Mouse fibroblast s

ALIGNMENTS

RESULT 1	
AA797142	
ID	AA797142 standard; cDNA, 1146 bp.
XX	
AC	AA797142;
DT	
XX	05-MAR-1998 (first entry)
DE	
XX	Human monocyte mature differentiation factor encoding cDNA.
XX	
KW	Human: monocyte; mature; differentiation factor; MMDP; macrophage
KM	cancer; immune activator; tissue culture; infectious disease; ds.
OS	
XX	Homo sapiens.
XX	
XX	
FH	Location/Qualifiers
FT	1..1146
FT	CDS
FT	/*tag= a
FT	/product= Monocyte_mature_differentiation_factor
PN	
XX	JP09234079-A.
XX	
PD	
XX	09-SEP-1997.
XX	
PF	04-MAR-1996; 96JP-0075236.
XX	
XX	04-MAR-1996; 96JP-0075236.
PR	
XX	(TUYM) TOYOBO KK.
XX	
XX	
WI	WI: 1997-497320/46.
DR	
DR	P-PSDE; AAW35957.

xx	A monocyte mature differentiation factor - useful for the long term
pt	tissue culture of macrophage(s)
xx	
ps	Claim 16; Page 13; 22pp; Japanese.
xx	
cc	The present sequence encodes a monocyte mature differentiation factor
cc	(MMDf) which maintains the life of macrophages for long periods in
cc	liquid culture. MMDf can be used as an anti-cancer agent, an immune
cc	activator and to treat infectious diseases.
xx	
s0	Sequence 1146 BP; 278 A; 325 C; 313 G; 230 T; 0 other;
Query Match	100.0%; Score 1146; DB 18; Length 1146;
Best Local Similarity	100.0%; Pred. No. 6,5e-301;
Matches 1146; Conservative	0; Mismatches 0; Indels 0; Gaps 0
Oy	1 ATGAGCTCCCGATGGCAGGCGCTGCCTTAAAGTCGTACACCCTTCCACTTTGACCAAG
Db	1 ATGAGCTCCCGATGGCAGGCGCTGCCTTAAAGTCGTACACCCTTCCACTTTGACCAAG
Oy	61 CTGGGCTCTCCACTGCCCGCTGCTGCCAATGCCCCCTTGAGAGGCCCAAGTGGCG
Db	61 CTGGGCTCTCTCACCTGCCCGCTGCTGCCAATGCCCCCTTGAGAGGCCCAAGTGGCG
Oy	121 CCGGAGTCGGGCTGCTCCGGAGGGCTGGCGCTGCTTAAGTGTGGCCCAAGACGTC
Db	121 CCGGAGTCGGGCTGCTCCGGAGGGCTGGCGCTGCTTAAGTGTGGCCCAAGACGTC
Oy	181 AACGAGACTCAGCAAAAACGACGCTGCGACACACACAAGGGCTGGAATGCAACTTC
Db	181 AACGAGACTCAGCAAAAACGAGGCTGCGACACACACAAGGGCTGGAATGCAACTTC
Oy	241 GGCGGCACTCCAGCGCTCTGTGAAGGGATTCTCAGAGCTCACTCAGAGGGCAGACCTGT
Db	241 GGCGGCACTCCAGCGCTCTGTGAAGGGATTCTCAGAGCTCACTCAGAGGGCAGACCTGT
Oy	301 GAATTAATCTCAGAAATCTACCAAAAAGGGGAAATTTCCAGGCCCACTGTAACATCAG
Db	301 GAATTAATCTCAGAAATCTACCAAAAAGGGGAAATTTCCAGGCCCACTGTAACATCAG
Oy	361 TGCAATGTATGTATGGCGCGGTGGGCTGCATTCCTCTGTGTGCCCAAGAATATCTCTC
Db	361 TGCAATGTATGTATGGCGCGGTGGGCTGCATTCCTCTGTGTGCCCAAGAATATCTCTC
Oy	421 CCCAATCTGGGCTCTGCCAACCTCTGGCTGTCAAAGTTACGGGCACTGCTGCAGAGAG
Db	421 CCCAATCTGGGCTCTGCCAACCTCTGGCTGTCAAAGTTACGGGCACTGCTGCAGAGAG
Oy	481 TGGGCTCTGACGAGTAGATATCATCAAGAACCCATGAGAGACAGAGAGGCTCCTTGGC
Db	481 TGGGCTCTGACGAGTAGATATCATCAAGAACCCATGAGAGAGAGAGGCTCCTTGGC
Oy	541 AAGGAGCTGGAGTTGATGCTCCGAGGTGAGAGTTGACGAGAAACAATGAATGTATGCA
Db	541 AAGGAGCTGGAGTTGATGCTCCGAGGTGAGAGTTGACGAGAAACAATGAATGTATGCA
Oy	601 GTTGGAAAAAGCAGCTCACTGAAGGGCTCCCTGTTTTGGAATGAGACCTGCATCTTA
Db	601 GTTGGAAAAAGCAGCTCACTGAAGGGCTCCCTGTTTTGGAATGAGACCTGCATCTTA
Oy	661 TACAACCTTTACAAGGCCAGAAATGTATTGTCCAACACTCTTCAGTGGCCAGAGTCGA
Db	661 TACAACCTTTACAAGGCCAGAAATGTATTGTCCAACACTCTTCAGTGGCCAGAGTCGA
Oy	721 AAGACCTGTGAACTGTATCTCCACACAGATTACCAATGACAAACCTGAGTGGCGCTT
Db	721 AAGACCTGTGAACTGTATCTCCACACAGATTACCAATGACAAACCTGAGTGGCGCTT
Oy	781 GTGAAGAAGAACCCGGATTTGTGAGGTGGCGCTTGTGACAGCCAGTGTACAGACGCTG
Db	781 GTGAAGAAGAACCCGGATTTGTGAGGTGGCGCTTGTGACAGCCAGTGTACAGACGCTG

QY	841	AAAAAGGCGAAGTAATGAGCAAGACCAAGAATAATCCCGGCAACGACGATTACTTAC	900
Db	841	AAAAAGGCGAAGTAATGAGCAAGACCAAGAATAATCCCGGCAACGACGATTACTTAC	900
QY	901	GCTGGATTTTGTAGTGTGTAAGAAATACCGGCCCAAGTACTGCGGTCTCGGTGACGCG	960
Db	901	GCTGGATTTTGTAGTGTGTAAGAAATACCGGCCCAAGTACTGCGGTCTCGGTGACGCG	960
QY	961	CGATGCTGCACGCCCCAGCTGACCAAGACTGTGAAGATGCGGTTCCCTGCGAAGATGG	1020
Db	961	CGATGCTGCACGCCCCAGCTGACCAAGACTGTGAAGATGCGGTTCCCTGCGAAGATGG	1020
QY	1021	GAGACATTTTCCAGAAACGTCATGATATCCACAGTCCTCGCAAAATGCACTACAAATGCGCG	1080
Db	1021	GAGACATTTTCCAGAAACGTCATGATATCCACAGTCCTCGCAAAATGCACTACAAATGCGCG	1080
QY	1081	CATGCCAATGAAAGCAGCGTTCCCTTCACAGCGTGTTCATTCATTCACAAATTTAGG	1140
Db	1081	CATGCCAATGAAAGCAGCGTTCCCTTCACAGCGTGTTCATTCATTCACAAATTTAGG	1140
QY	1141	GACTAA 1146	
Db	1141	GACTAA 1146	
RESULT 2			
ID	AAD29095	standard; cDNA; 1146 BP.	
AC	AAD29095;		
DT	07-MAY-2002	(first entry)	
DE	Human connective tissue growth factor-2 (CTGF-2) cDNA.		
KW	Human; angiogenesis; connective tissue growth factor-2; CTGF-2; tumour; ischaemia; restenosis; tissue repair; wound healing; congenital defect; cardiovascular disease; atherosclerosis; heart failure; angina; trauma; burns; osteoporosis; periodontal disease; liver failure; transquillizer; vulnerability; cosmetic plastic surgery; vasotropic; hepatotropic; ulcer; gene therapy; ss.		
OS	Homo sapiens.		
XX	Key	Location/Qualifiers	
XX	CDS	1..1146	
XX	FT	/*tag= a	
XX	FT	/product= "Human CTGF-2"	
XX	WO200204480-A2.		
XX	17-JAN-2002.		
XX	11-JUL-2001; 2001WO-US21799.		
XX	11-JUL-2000; 2000US-217402P.		
XX	18-MAY-2001; 2001US-291642P.		
XX	(HUMA-) HUMAN GENOME SCI INC.		
XX	(TRGE) TRANSGENE SA.		
XX	Li H, Adams MD, Calenda V, Fatuccioli V;		
XX	WPI; 2002-171698/22.		
XX	P-PSDB; AAE18107.		
XX	Stimulating angiogenesis in a mammal preferably human having ischemia or restenosis or is treated for limb revascularization, by administering connective tissue growth factor-2 polypeptide or polynucleotide -		
XX	Example 1; Fig 1; 131pp; English.		

CC The present invention relates to a method for stimulating angiogenesis in
 CC a mammal. The method comprises administering a polynucleotide encoding
 CC connective tissue growth factor-2 (CTGF-2) or an active fragment or its
 CC derivative. The method is useful for stimulating angiogenesis in a mammal
 CC preferably human having ischemia or restenosis or is treated for limb
 CC revascularisation which is leg or arm. The invention is useful for
 CC inhibiting tumour growth, where angiogenesis is utilised for enhancing
 CC the repair of connective tissue and support tissue, promoting the attachment,
 CC fixation and stabilisation of tissue implants and enhancing wound
 CC healing, hence is useful for treating cardiovascular disease e.g.
 CC atherosclerosis, reperfusion injury such as heart failure, angina,
 CC ischaemia, and is also used to differentiate, proliferate and attract
 CC cells leading to regeneration of tissues which is utilised to repair
 CC replace or protect tissue damaged by congenital defects, trauma (burns,
 CC ulcer, etc), age, disease (e.g. osteoporosis, periodontal disease,
 CC liver failure), surgery including cosmetic plastic surgery. The present
 CC sequence is human CTGF-2 cDNA. CTGF-2 gene is useful in gene therapy.
 CC
 XX
 S0 Sequence 1146 BP; 278 A; 325 C; 313 G; 230 T; 0 other;

Query Match 100.0%; Score 1146; DB 24; Length 1146;
 Best Local Similarity 100.0%; Pred. No. 6.5e-301; Mismatches 0; Gaps 0;
 Matches 1146; Conservative 0; Indels 0;

QY 1 ATGAGCTCCCGCATCGCCAGGCGCTGCTAGTCTGTCACCTTCTTCACCTTACAGCAGG 60
 DB 1 ATGAGCTCCCGCATCGCCAGGCGCTGCTAGTCTGTCACCTTCTTCACCTTACAGCAGG 60
 QY 61 CTGGCGCTTCACCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 120
 DB 61 CTGGCGCTTCACCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 120
 QY 121 CCGGAGCTCGGCGCTGCTGCGGAGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
 DB 121 CCGGAGCTCGGCGCTGCTGCGGAGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
 QY 181 AAGCAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
 DB 181 AAGCAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
 QY 241 GCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 DB 241 GCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 QY 301 GAATATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
 DB 301 GAATATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
 QY 361 TGCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
 DB 361 TGCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
 QY 421 CCCAATCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
 DB 421 CCCAATCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
 QY 481 TGGGCTGTGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
 DB 481 TGGGCTGTGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
 QY 541 AAGGAGCTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 DB 541 AAGGAGCTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 QY 601 GTTGGAAAAAGCAGTCACTGAGAGGCTCCCTGTTTGGAAATGAGACCTCGCATCTCTA 660
 DB 601 GTTGGAAAAAGCAGTCACTGAGAGGCTCCCTGTTTGGAAATGAGACCTCGCATCTCTA 660
 QY 661 TACAACTTTTACAAAGCCAGAAATGATGTTGTTCAAAACATTCATGTTCCAGAGCTCA 720
 DB 661 TACAACTTTTACAAAGCCAGAAATGATGTTGTTCAAAACATTCATGTTCCAGAGCTCA 720
 QY 721 AAGACCTGTGAACTGTATCTCCACAGAGTTACCAATGACACCTGAGTGCCTT 780

DB 721 AAGACCTGTGAACTGTATCTCCACAGAGTTACCAATGACACCTGAGTGCCTT 780
 QY 781 GTGAAAACAAACCCGATTTTGTAGGTGCGGCTTTGTGACAGCAGTGTACAGCAGCTG 840
 DB 781 GTGAAAACAAACCCGATTTTGTAGGTGCGGCTTTGTGACAGCAGTGTACAGCAGCTG 840
 QY 841 AAAAAGGGCAAGAAATCAGACAGACCAAGAAATCCCGGACAGCAGTGTACTTAC 900
 DB 841 AAAAAGGGCAAGAAATCAGACAGACCAAGAAATCCCGGACAGCAGTGTACTTAC 900
 QY 901 GCTGATGTTTGTAGTGTGAAGAAATACCGGCCCAAGTACTGCGTTCTCGTGGACGCG 960
 DB 901 GCTGATGTTTGTAGTGTGAAGAAATACCGGCCCAAGTACTGCGTTCTCGTGGACGCG 960
 QY 961 CGATGCTGACGCCCCGAGCTGACAGACACTGTGAAGTGGGTTCCGCTCGGAAGTGG 1020
 DB 961 CGATGCTGACGCCCCGAGCTGACAGACACTGTGAAGTGGGTTCCGCTCGGAAGTGG 1020
 QY 1021 GAGCATTTTCCAGAAAGTCATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
 DB 1021 GAGCATTTTCCAGAAAGTCATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
 QY 1081 CATGCCAATGAGCAGGCTTCCCTCTACAGGCTGTTCATGACATTCACAAATTTAGG 1140
 DB 1081 CATGCCAATGAGCAGGCTTCCCTCTACAGGCTGTTCATGACATTCACAAATTTAGG 1140
 QY 1141 GACTTA 1146
 DB 1141 GACTTA 1146

RESULT 3
 ABR48899 standard; DNA; 1418 BP.
 ID ABR48899 standard; DNA; 1418 BP.
 AC ABR48899;
 XX
 DT 30-JUL-2002 (first entry)
 XX
 DE DNA encoding human Cyr61.
 XX
 KW Human; uterine leiomyoma proliferation; uterine leiomyoma formation;
 KW Cyr61; cytoskeletal; gene; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 124..1269
 FT /*tag= a
 FT /product= "Cyr61"
 XX
 PN W0200226193-A2.
 XX
 PD 04-APR-2002.
 XX
 PE 28-SEP-2001; 2001WO-US30783.
 XX
 PR 29-SEP-2000; 2000US-236887P.
 XX
 PA (AMHP) AMERICAN HOME PROD CORP.
 PI Zhang Z, Sampath D, Zhu Y, Winneker R.
 XX
 DR WPI: 2002-383245/41.
 DR P-PSDB: MAU79761.
 XX
 PT Preventing uterine leiomyoma formation or inhibiting proliferation of
 PT uterine leiomyoma in subject, comprises modulating or increasing the
 PT level of Cyr61 in leiomyoma tissue
 XX
 PS Disclosure; Fig 6; 92pp; English.
 XX

CC The present invention relates to a method of inhibiting proliferation
 CC of uterine leiomyoma or preventing uterine leiomyoma formation. The
 CC method comprises increasing the level of Cyr61 in leiomyoma tissue.
 CC The invention also describes compounds and compositions that stimulate
 CC induction of the Cyr61 gene and compounds that increase Cyr61 activity.
 CC The compositions and the method of the invention are useful for
 CC preventing uterine leiomyoma formation or inhibiting proliferation of
 CC uterine leiomyoma in a subject. The method is particularly useful for
 CC treating or preventing uterine leiomyoma formation, or inhibiting
 CC proliferation of uterine leiomyoma in a subject. The present sequence
 CC encodes human Cyr61.
 CC Note: The present sequence shown in Fig 6 is not shown in the correct
 CC sequence order in the figure. The start of the sequence is shown on
 CC page 8/10 of the figures, and the rest of the sequence is shown on
 CC pages 6/10 and page 7/10 of the figures.
 CC
 XX Sequence 1418 BP; 334 A; 407 C; 398 G; 279 T; 0 other;
 Query Match 100.0%; Score 1146; DB 24; Length 1418;
 Best Local Similarity 100.0%; Pred. No. 7,1e-301;
 Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGAGCTCCCGACGCGGCGGCTGCGCTTGTGCTACCTCTCCACTTGACAGG 60
 DB 124 ATGAGCTCCCGACGCGGCGGCTGCGCTTGTGCTACCTCTCCACTTGACAGG 183
 QY 61 CTGGCGCTCTCAGCTGCGCGGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGG 120
 DB 184 CTGGCGCTCTCAGCTGCGCGGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGG 243
 QY 121 CCGGGAGTGGGGTGGTCCGGGAGCGGTGCGGTGCTGTAGGTCTCCGCAAGCAGCTC 180
 DB 244 CCGGGAGTGGGGTGGTCCGGGAGCGGTGCGGTGCTGTAGGTCTCCGCAAGCAGCTC 303
 QY 181 AAGGAGGAGCTGACGAGAAAGCGAGCCCTGCGACACACCAAGGGGCTGGAATGCACTTC 240
 DB 304 AAGGAGGAGCTGACGAGAAAGCGAGCCCTGCGACACACCAAGGGGCTGGAATGCACTTC 363
 QY 241 GCGCGGAGCTGACGCGGCTGGAAGGGGAGTCTGAGAGCTCAGTACAGAGGCGAGCCCTGT 300
 DB 364 GCGCGGAGCTGACGCGGCTGGAAGGGGAGTCTGAGAGCTCAGTACAGAGGCGAGCCCTGT 423
 QY 301 GAATATACGCAAGATCTACCAAAAGGGGGAAGTTCCAGGCCCACTTAAACATACAG 360
 DB 424 GAATATACGCAAGATCTACCAAAAGGGGGAAGTTCCAGGCCCACTTAAACATACAG 483
 QY 361 TGCACATGATATGATGGCGGCTGCGCTGCTCTGTCTGCTCCCAAGAACTATCTCTC 420
 DB 484 TGCACATGATATGATGGCGGCTGCGCTGCTCTGTCTGCTCCCAAGAACTATCTCTC 543
 QY 421 CCCAACTGGGGCTGCTCCCAACCTCGGCTGCTGCTCAAAAGTTACCGGGCAGTCTCGAGAG 480
 DB 544 CCCAACTGGGGCTGCTCCCAACCTCGGCTGCTGCTCAAAAGTTACCGGGCAGTCTCGAGAG 603
 QY 481 TGGGTCTGTGAGAGATAGTATCAGAGGCCCATGAGAGACCGAGGCGCTCTTGGC 540
 DB 604 TGGGTCTGTGAGAGATAGTATCAGAGGCCCATGAGAGACCGAGGCGCTCTTGGC 663
 QY 541 AAGGAGCTGGGATTCATGCTCCGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAG 600
 DB 664 AAGGAGCTGGGATTCATGCTCCGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAG 723
 QY 601 GTTGAAGGAGGAGCTCAGTGAAGGGGCTCCTGTTTTTGGAAATGAGGCTCGCATCTCA 660
 DB 724 GTTGAAGGAGGAGCTCAGTGAAGGGGCTCCTGTTTTTGGAAATGAGGCTCGCATCTCA 783
 QY 661 TACAACCTTTAAGGCGCAAGATGATTTTCTCAACAACTTCATGCTCCAGTCTCA 720
 DB 784 TACAACCTTTAAGGCGCAAGATGATTTTCTCAACAACTTCATGCTCCAGTCTCA 843
 QY 721 AAGAGCTGTGAGACTGTATCTCCACAGAGGTACCAATGACAAACCTGAGTGGCGGCTT 780
 DB 844 AAGAGCTGTGAGACTGTATCTCCACAGAGGTACCAATGACAAACCTGAGTGGCGGCTT 903

QY 781 GTGAAGAAACCCGGATTTGTGAGTGGCGCTTGTGACAGCCAGTGTACAGACGCTG 840
 DB 904 GTGAAGAAACCCGGATTTGTGAGTGGCGCTTGTGACAGCCAGTGTACAGACGCTG 963
 QY 841 AAAAGGCAAGAAATGACAGCAAGCAAGAAATCCCGGAAACAGTCAAGTTACTTAC 900
 DB 964 AAAAGGCAAGAAATGACAGCAAGCAAGAAATCCCGGAAACAGTCAAGTTACTTAC 1023
 QY 901 GCTGAGATTTTGTGAGTGAAGAAATACCGGCCCACTAGTGGGCTTCTGCGGAGCGG 960
 DB 1024 GCTGAGATTTTGTGAGTGAAGAAATACCGGCCCACTAGTGGGCTTCTGCGGAGCGG 1083
 QY 961 CGATGCTGACAGCGCCAGCTGACAGGAGTGTGAAGATGCGGTTCGTCGCAAGATGGG 1020
 DB 1084 CGATGCTGACAGCGCCAGCTGACAGGAGTGTGAAGATGCGGTTCGTCGCAAGATGGG 1143
 QY 1021 GAGACATTTTCCAAAGACGTCATGATGATTCAGTCTCGCAATGCACTACAAATTTAGG 1080
 DB 1144 GAGACATTTTCCAAAGACGTCATGATGATTCAGTCTCGCAATGCACTACAAATTTAGG 1203
 QY 1081 CATGCCAATGAAGACAGCTTCCCTCTACAGGCTGTCAATGATTCACAAATTTAGG 1140
 DB 1204 CATGCCAATGAAGACAGCTTCCCTCTACAGGCTGTCAATGATTCACAAATTTAGG 1263
 QY 1141 GACTAA 1146
 DB 1264 GACTAA 1269

RESULT 4
 ABA93130
 ID ABA93130 standard; cDNA; 1419 BP.

XX ABA93130;

DT 15-APR-2002 (first entry)

XX Human Cyr61 protein encoding cDNA.

DE Human: Cyr61; breast cancer; sex steroid receptor; cytosolic; promoter;

KW sex steroid response element; cysteine rich heparin-binding protein;

KW cell proliferation; heparin binding epidermal growth factor;

KW epidermal growth factor; basic fibroblastic growth factor; gene; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS /tag 124..1269

FT /product= "Cyr61 protein"

PD WO200198359-A2.

XX 27-DEC-2001.

XX 21-JUN-2001; 2001WO-US19823.

XX 21-JUN-2000; 2000US-213182P.

PR 16-MAY-2001; 2001US-291510P.

XX (AMHP) AMERICAN HOME PROD CORP.

PA Sampath D, Zhang Z, Wineker R;

DR WPI: 2002-147796/19.

XX P-PSDB; ABB05438.

PT Regulation of Cyr61 expression and activity for preventing and

inhibiting breast cancer comprises use of a Cyr61 neutralizing

antibody, an anti-sense oligonucleotide and an antibody which

disclosure: Fig 2A-C; 86pp; English.

xx The present invention describes a method for the prevention or inhibition of breast cancer cell proliferation. The method comprises administration of a compound that inhibits the interaction of a sex steroid receptor with a sex steroid response element of the Cyt61 (cysteine rich heparin-binding protein) promoter. Cyt61 has cytostatic activity. An antibody (I) which neutralises Cyt61 can be used to prevent or inhibit breast cancer cell proliferation by blocking sex steroid induced and growth factor induced synthesis of Cyt61 DNA, where the growth factor is epidermal, heparin binding epidermal or basic fibroblastic growth factor. (I) can be used to diagnose or stage breast cancer where the level of Cyt61 in a positive/suspect breast cancer cell is compared to the level in a normal cell, an increase in the level of Cyt61 compared to the level in normal tissue indicates the presence of breast cancer. The level of Cyt61 being determined by exposing the tissues to (I), and an increase in the level of bound antibody by the suspect/positive cell as compared to the normal tissue indicates the presence of breast cancer. The present sequence encodes the human Cyt61 protein, which is used in the exemplification of the present invention.

xx Sequence 1419 BP; 334 A; 407 C; 399 G; 279 T; 0 other;

Query Match 100.0%; Score 1146; DB 24; Length 1419;

Best Local Similarity 100.0%; Pred. No. 7.1e-301;

Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGAGCTCCGCGATCGGCGGCGGCGCTGAGTGCACCTTCTCCACTTGACGAG 60
 124 ATGAGCTCCGCGATCGGCGGCGGCGCTGAGTGCACCTTCTCCACTTGACGAG 183
 61 CTGGCGCTCTCCACTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
 184 CTGGCGCTCTCCACTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 243
 121 CCGGAGTGGGCTGGTGGGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
 244 CCGGAGTGGGCTGGTGGGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 303
 181 AAGCAGCTGCGAGCAAAAGCAGCCTGCGAGCAACCAAGGCGGAGTGAATGCACTTC 240
 304 AAGCAGCTGCGAGCAAAAGCAGCCTGCGAGCAACCAAGGCGGAGTGAATGCACTTC 363
 241 GGGCGCAGCTCCACCGCTGCGAGGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 300
 364 GGGCGCAGCTCCACCGCTGCGAGGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 423
 301 GAATATTAATCTCAAGATCTACCAAAAGGGAAGTTCCAGCCCACTGTAACATCAG 360
 424 GAATATTAATCTCAAGATCTACCAAAAGGGAAGTTCCAGCCCACTGTAACATCAG 483
 361 TGCAATGATTTGATGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 484 TGCAATGATTTGATGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 543
 421 CCCAATTTGGCTGTCCCAACCTCGGCTGTCAAAAGTTACCGGGCACTGCTGAGAGAG 480
 544 CCCAATTTGGCTGTCCCAACCTCGGCTGTCAAAAGTTACCGGGCACTGCTGAGAGAG 603
 481 TGGGCTGTGAGAGGAGTATATCAAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 604 TGGGCTGTGAGAGGAGTATATCAAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 663
 541 AAGGAGCTGGATTCGATGCTCGAGAGTGAAGTGAAGAGAGAGAGAGAGAGAGAGAG 600
 664 AAGGAGCTGGATTCGATGCTCGAGAGTGAAGTGAAGAGAGAGAGAGAGAGAGAGAG 723
 601 GTTGGAG 660
 724 GTTGGAG 783
 661 TACAACCTTTACAG 720
 784 TACAACCTTTACAG 843

QY 721 AAGACTGTGGAAGTGTATCTCCACAGAGATTACCAATGACAACTGAGTGGCGCTT 780
 DB 844 AAGACTGTGGAAGTGTATCTCCACAGAGATTACCAATGACAACTGAGTGGCGCTT 903
 QY 781 GTGAAAGAAACCCGGAATTTGTGAGGTGCGGCTTTGTGAGACAGCCAGTGTACAGCAGCTG 840
 DB 904 GTGAAAGAAACCCGGAATTTGTGAGGTGCGGCTTTGTGAGACAGCCAGTGTACAGCAGCTG 963
 QY 841 AAAAAGGCAAGAAATGACAG 900
 DB 964 AAAAAGGCAAGAAATGACAG 1023
 QY 901 GCTGATGTTGAGTGTGAAGAAATACCGGCGCAAGTACTGCTGCTGCTGCTGCTGCTG 960
 DB 1024 GCTGATGTTGAGTGTGAAGAAATACCGGCGCAAGTACTGCTGCTGCTGCTGCTGCTG 1083
 QY 961 CGATGCTGACAGCCCGAGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
 DB 1084 CGATGCTGACAGCCCGAGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1143
 QY 1021 GAGACATTTTCCAG 1080
 DB 1144 GAGACATTTTCCAG 1203
 QY 1081 CATGCCAATGAG 1140
 DB 1204 CATGCCAATGAG 1263
 QY 1141 GACTAA 1146
 DB 1264 GACTAA 1269

RESULT 5
 AAH02896
 ID AAH02896 standard; DNA; 2016 BP.

XX AAH02896;
 XX 15-JUN-2001 (first entry)
 DE Human shear stress-response coding sequence SPO ID NO: 45.
 XX Human; shear stress-response protein; vascular disease;
 KW arteriosclerosis; ds.
 OS Homo sapiens.
 PN WO200125427-A1.
 PD 12-APR-2001.
 PE 02-OCT-2000; 2000WO-JP06840.
 PR 01-OCT-1999; 99JP-0280976.
 PA (KYOM) KYOMA HAKKO KOYO KK.
 PA (NOI/) NOJIMA H.
 PI Nojima H, Yoshisue H, Obayashi M, Ota T, Kawabata A, Sakurada K;
 PI Kuga T, Sekine S, Nakamura Y, Sugano S;
 DR WPI: 2001-266308/27.
 DR P-PSDB: AAB90773.
 XX DNA sequences, proteins encoded by them and antibodies against them
 PT useful in diagnosis and treatment of vascular disease caused by
 PT arteriosclerosis -
 XX Claim 20; Page 341-344; 678bp; Japanese.
 CC The present invention provides the protein and coding sequences of a

CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

Sequence 2016 BP; 490 A; 525 C; 534 G; 467 T; 0 other;

Query Match	100.0%	Score 1146	DB 24	Length 2016
Best Local Similarly	100.0%	Pred. No. 8.3e-301		
Matches 1146	0	Mismatches 0	Indels 0	Gaps 0

OY	ATGAGCTCCCGCAATCGGCAGAGGAGCCTGACCTTATGTCACACCTTTCACCTTGACACG	60
Db	ATGAGCTCCCGCAATCGGCAGAGGAGCCTGACCTTATGTCACACCTTTCACCTTGACACG	210
OY	CTGAGCCTCTCCACTCTGCCCGCTGACCTGACCTGACCGCCCTGAGAGGCCAATGCGCG	61
Db	CTGAGCCTCTCCACTCTGCCCGCTGACCTGACCTGACCGCCCTGAGAGGCCAATGCGCG	270
OY	CCGGGAAGTCGGGCTGTGTCCGGGACGCGTCGGGCTGTGTAAAGTCTGCGCCAMCAGCTC	121
Db	CCGGGAAGTCGGGCTGTGTCCGGGACGCGTCGGGCTGTGTAAAGTCTGCGCCAMCAGCTC	330
OY	AAGAGGAGCTGACCAAAAGCAGCAGCCCGGAGCCACACCAAGAGGGGCTGGAATGCACTTC	181
Db	AAGAGGAGCTGACCAAAAGCAGCAGCCCGGAGCCACACCAAGAGGGGCTGGAATGCACTTC	390
OY	GGCGCCAGCTCCACCGCTCTGTAAGGGATCTGCAGACTCAGTACAGAGGGCAGACCTGT	241
Db	GGCGCCAGCTCCACCGCTCTGTAAGGGATCTGCAGACTCAGTACAGAGGGCAGACCTGT	450
OY	GAATATTAATCTCAGAAATCTACCAAAACGGGAAAGTTCCAGCCCACTGTAACATCAG	301
Db	GAATATTAATCTCAGAAATCTACCAAAACGGGAAAGTTCCAGCCCACTGTAACATCAG	510
OY	TGCACATGATTAATGAGCGCGCGTGGGCGCATTCCTCTGCTGCCCAAGAACTATCTCTC	361
Db	TGCACATGATTAATGAGCGCGCGTGGGCGCATTCCTCTGCTGCCCAAGAACTATCTCTC	570
OY	CCCAACTTGGGCTTCCCAACCTCTGCGCTGTCTCAAAATTAACGGGCAAGTCGAGAGAG	421
Db	CCCAACTTGGGCTTCCCAACCTCTGCGCTGTCTCAAAATTAACGGGCAAGTCGAGAGAG	630
OY	TGGCTCTGTGACGAGATAGTATCAAGAGACCCCATGAGAGACCGAGCGCTCTTGGC	481
Db	TGGCTCTGTGACGAGATAGTATCAAGAGACCCCATGAGAGACCGAGCGCTCTTGGC	690
OY	AAGAGGCTGGGATTCGATCCCTCCGAGGTGAGTGTGAAGAGAAACATGATTTATTTGCA	541
Db	AAGAGGCTGGGATTCGATCCCTCCGAGGTGAGTGTGAAGAGAAACATGATTTATTTGCA	750
OY	GTTGGAAAAGGACAGCTCACTGAACGGGCTCCCTTTTGGAAATGGAAGCCCTGCATCTTA	601
Db	GTTGGAAAAGGACAGCTCACTGAACGGGCTCCCTTTTGGAAATGGAAGCCCTGCATCTTA	810
OY	TACAAACCTTTACAAAGGCCAGAAATGTAATTTGTTAAACAACTCATGCTGCCAGTCTCA	661
Db	TACAAACCTTTACAAAGGCCAGAAATGTAATTTGTTAAACAACTCATGCTGCCAGTCTCA	870
OY	AAGACCTGTGAACTGTAATCTCCACACAGATTTACCAATGTCAACCTGATGTGCCCTT	721
Db	AAGACCTGTGAACTGTAATCTCCACACAGATTTACCAATGTCAACCTGATGTGCCCTT	930
OY	GTGAAGCAAAACCCGGAATTTGTGAGGTGGGCTTGTGAGACGCCAGTGTACAGAGCCTG	781
Db	GTGAAGCAAAACCCGGAATTTGTGAGGTGGGCTTGTGAGACGCCAGTGTACAGAGCCTG	990
OY	AAAAAGGCAAGAAATGCAGCAAGACCAAGAAATCCCCGGAACGATCAGGTTTACTTAC	841
Db	AAAAAGGCAAGAAATGCAGCAAGACCAAGAAATCCCCGGAACGATCAGGTTTACTTAC	1050
OY	GCTGGATGTTTGAATGTGAAAGAAATTACCGGCCCAAGTACTCGGTTCTCGGTGTGAGAGGC	901
Db	GCTGGATGTTTGAATGTGAAAGAAATTACCGGCCCAAGTACTCGGTTCTCGGTGTGAGAGGC	1110

Accession	Sequence	Position
QY	CGATGCTGACAGCCGCCACACTATACAGACGCTGTGAAGATGGCGTTCCGCTGGGAAGATGG	1020
QY		
Db	CGATGCTGACAGCCGCCACACTATACAGACGCTGTGAAGATGGCGTTCCGCTGGGAAGATGG	1229
QY	1021 GAGACATTTTCCAGAAACGTCATGATGATTCACGTCCTGCAATGCAACTACATACATGCCCG	1080
QY		
Db	1230 GAGACATTTTCCAGAAACGTCATGATGATTCACGTCCTGCAATGCAACTACATACATGCCCG	1289
QY	1081 CATGCCAATGAGACGCGTTTCCTTCTACAGSCTGTTCAAATGACATTCACAAATTAGG	1140
QY		
Db	1290 CATGCCAATGAGACGCGTTTCCTTCTACAGSCTGTTCAAATGACATTCACAAATTAGG	1349
QY	1141 GACTTAA 1146	
QY		
Db	1350 GACTTAA 1355	

RESULT	7
ABK64742	
ID	ABK64742 standard; DNA; 2016 BP.
XX	
AC	ABK64742;
XX	
DT	18-JUN-2002 (first entry)

DE Human benign prostatic hyperplasia gene #637.

OS Homo sapiens.

PN WO200212440-A2

PD 14-FEB-2002.

PF 07-AUG-2001; 2001WO-US24708.

PR 07-AUG-2000; 2000US-223323P

XX

PA (NISB) JAPAN TOBACCO INC.

PI Munger WE, Kulkarni P, C

DR WPI; 2002-257476/30.

PT Identifying drugs for

PT patient that are differentially regulated compared to normal prostate PT cells -

PS Disclosure; Page 347; 444pp; English.

The invention relates to a method of diagnosing (I) the onset or progression of benign prostatic hyperplasia (BPH), or screening (II) for or identifying an agent that modulates the onset or progression of BPH, or identifying an agent that modulates the onset or progression of BPH. The method is based on changes in gene expression in BPH tissue. Isolated from patients exhibiting different clinical states of prostate hyperplasia as compared to normal prostate tissue. (I) comprises detecting the expression levels of one or more genes in prostate cells from the subject that are differentially regulated compared to normal prostate cells. (II) comprises preparing a first gene expression profile of BPH cells or BPH-like cell population, exposing the cells to the agent, preparing a second gene expression profile of the agent exposed cells, and comparing the first and second gene expression profiles. (I) is useful for diagnosing the onset or progression of BPH. (II) is useful for identifying an agent that modulates the onset or progression of BPH. The methods are useful to prevent information identifying the expression level in a tissue or cells, by comparing the expression level of genes given in the specification in the tissue or cells to the level of expression of gene in the database, and displaying the

PR Screening for anti-neoplastic agent involves exposing cells to a
PT chemical agent to be tested for anti-neoplastic activity, and
PR determining a change in expression of a gene of a signature gene set
XX
PS Claim 1; SEQ ID 6895; 44pp; English.

CC The present invention describes a method (M1) for screening for an
CC anti-neoplastic agent. The method involves exposing cells to a chemical
CC agent to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in AB165164
CC to AB170110), or is at least 93% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophagaeal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilms' tumour.

Sequence 2016 BP; 490 A; 525 C; 534 G; 467 T; 0 other;

Query Match	100.08;	Score 1146;	DB 24;	Length 2016;
PostgreSQL C:\Program Files\Microsoft SQL Server\90\Tools\Binn\sqlcmd.exe	100.08	Score 1146	DB 24	Length 2016

Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCCTTCTCCACTTGACCAGG 60

Db 210 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTGTGTCACCCCTTCTCCACTTGACCAGG 269

QY 61 CTGGCGCTCTCCACCTGCCCGCTGCCCTGCCACTGCCCGCTGGAGGCGCCCAAGTGGCG 120

Db 270 CTGGCGCTCTCCACCTGCCCCGCTGCCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGGCG 329

QY 121 CCGGAGTCGGGCTGTCGGGACGGCTGCGGCTGTAAGTCTGCGCCAAAGCAGCTC 180

Db 330 CCGGAGTCCGGGCTGCTCCGGGACGGCTGCGGCTGTAAGGTCGCGCAAGCAGCTC 389

Ox 181 AAGGAGCACTGCACCAACAAGCACCACAAACCCACTCACCATTCACATTAACAATAA
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QY	361	GGCAGATGATTAATGAGCGCGTGGGCGATTCCTCGTGTGTCCCGCAAGAACTATCCTC	420
Db	570	TGCACATGATATTATGGCGCCGTGGCTGCATTCCTCTGTGTGCCCAAGAACTATCTCTC	629
QY	421	CCCAAGTTGGGCTGTCCCAACCCGTGGTGGTCAAAAGTTACCGGGGCACTGCTGCAGAGAG	480
Db	630	CCCACATTGGGCTGTCCCAACCCGTGGTGGTCAAAAGTTACCGGGGCACTGCTGCAGAGAG	689
QY	481	TGGTCTGTGCAGAGATAGTATCAAGACCCCATGGAGGACCAAGGAGCGCTCCTTGGC	540
Db	690	TGGTCTGTGCAGAGATAGTATCAAGGACCCCATGGAGGACCAAGGAGCGCTCCTTGGC	749
QY	541	AAGAGCTGGGATTCGATGCTCCGAGGTGGAGTTGACGAAACAAATGAATTGATTGCA	600
Db	750	AAGAGCTGGGATTCGATGCTCCGAGGTGGAGTTGACGAAACAAATGAATTGATTGCA	809
QY	601	GTGTGAAAGGACGCTCACTGAAGCGGCTCCTGTTTTGGAAATGGAACCTCGCATCCTA	660

QY 661 TACAACCCCTTACAAGGCGACAATGTAATGTTCTCAAAACAACCTCATGTCACGATGCTCA 720
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870 TACAACCCCTTACAAGGCGACAATGTAATGTTCTCAAAACAACCTCATGTCACGATGCTCA 929
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[illegible]

041 *****13CAGCAGAGACAGAGAA1CCCCAGACCG1CAGG11AC11AC 500

DB 1050 AAAAAGGCGCAAGAAATGCGCAGACCAAGAAATCCCCGGAACGATCAGGTTACTAC 1105

901 GCCTGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACCTGGGGTTCCTGCGTGGACGGC 960

DB 1110 GCCTGGATGTTTGAGTGTGAGAAATACCGGCCCAAGTACCTGCCGTCCGCGACGCC 1165

961 CGATGCTGCACGCCCCAGCTGACCAAGACCTGTGAAGATGGGTCCGCTCCGAAGATGGG 1020

DB 1170 CGATGCTGCACGCCCCCAGCTGACCAGGACTGTGAAGATGCCGTTCCGCTGCCGAAGATGGC 1223

1021 GAGACATTTTCCAAGAACGTCATGATCCAGTCTGCAATGCAACTACCACTGCCCG 1080

Db 1230 GAGACATTTTCCAGAAGCTCATGATGATCCAGTCTGCAATGCAACTACCACTGCCCG 1289

1081 CATGCCAATGAGCAGCGTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTAGG 1140

Db 1290 CATGCCAATGAAGCAGCGTTCCCTTCTACAGGCTGTTCAATGACATTCAACAATTAGG 1349

QY 1141 GACTAA 1146

Db 1350 GACTAA 1355

NEEDLE 2
ABA93127

ADRESSE / SCALAIRE, CDM, 2010 DE.
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AC
ABW9312/;

DT 13-APR-2002 (first entry)
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Human Cyr61 protein encoding cDNA SEQ ID NO:1.

KW Human; Cyr61; breast cancer; sex steroid receptor; cytostatic; promoter;

cell proliferation; heparin binding epidermal growth factor;

XX

XX Key Location/Qualifiers
 FH CDS 210..1355
 FT /tag- a
 FT /product- "Cyr61 protein"
 XX MO200198359-A2.
 PN
 PD 27-DEC-2001.
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 PF 21-JUN-2001; 2001MO-US19823.
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 PR 21-JUN-2000; 2000US-213182P.
 XX 16-MAY-2001; 2001US-291510P.
 XX
 PA (AMHP) AMERICAN HOME PROD CORP.
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 PI Sampath D, Zhang Z, Winneker R;
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 DR WPI; 2002-147796/19.
 DR P-PSDB; ABB05438.
 XX
 PT Regulation of Cyr61 expression and activity for preventing and
 PT inhibiting breast cancer comprises use of a Cyr61 neutralizing
 PT antibody, an anti-sense oligonucleotide and an antibody which
 XX
 PS Disclosure; Page 84-85; 86pp; English.
 XX
 CC The present invention describes a method for the prevention or inhibition
 CC of breast cancer cell proliferation. The method comprises administration
 CC of a compound that inhibits the interaction of a sex steroid receptor
 CC with a sex steroid response element of the Cyr61 (cysteine rich heparin-
 CC binding protein) promoter. Cyr61 has cytosolic activity. An antibody (I)
 CC which neutralises Cyr61 can be used to prevent or inhibit breast cancer
 CC cell proliferation by blocking sex steroid induced and growth factor
 CC induced synthesis of Cyr61 DNA, where the growth factor is epidermal,
 CC heparin binding epidermal or basic fibroblastic growth factor. (I) can be
 CC used to diagnose or stage breast cancer where the level of Cyr61 in a
 CC positive/suspect breast cancer cell is compared to the level in a
 CC normal cell, an increase in the level of Cyr61 compared to the level in
 CC normal tissue indicates the presence of breast cancer. The level of
 CC Cyr61 being determined by exposing the tissues to (I), and an increase
 CC in the level of bound antibody by the suspect/positive cell as compared
 CC to the normal tissue indicates the presence of breast cancer. The present
 CC sequence encodes the human Cyr61 protein, which is used in the
 CC exemplification of the present invention.
 CC
 XX
 SQ Sequence 2016 BP; 490 A; 525 C; 534 G; 467 T; 0 other;

Query Match 100.0%; Score 1146; DB 24; Length 2016;
 Best Local Similarity 100.0%; Pred. No. 8.3e-301;
 Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGAGCTCCCGCATGCGGAGGCGCTGAGTGCACCTTCCACTTGAACAGG 60
 210 ATGAGCTCCCGCATGCGGAGGCGCTGAGTGCACCTTCCACTTGAACAGG 269
 61 CTGGGCTCTCCACTGCGGCGCTGCTGCCTGCACTGCCCCCTGAGAGCGGCCAAAGTGGCG 120
 270 CTGGGCTCTCCACTGCGGCGCTGCTGCCTGCACTGCCCCCTGAGAGCGGCCAAAGTGGCG 329
 121 CCGGAGTCTGGGCTGCTCGGAGAGGCTGCGGCTGCTGTAAGTCTGCGCCCAAGCAAGCTC 180
 330 CCGGAGTCTGGGCTGCTCGGAGAGGCTGCGGCTGCTGTAAGTCTGCGCCCAAGCAAGCTC 389
 181 AAGGAGACTGAGCAAAAACGAGCCCTGCGACACACACAAAGGGCTGGAAATGCAACTTC 240
 390 AAGGAGACTGAGCAAAAACGAGCCCTGCGACACACACAAAGGGCTGGAAATGCAACTTC 449
 241 GGCGGCACTCCACCGCTCTGAAGGGAATCTGCAGAGCTCACTCAGAGGCGAGACCTGT 300
 450 GGCGGCACTCCACCGCTCTGAAGGGAATCTGCAGAGCTCACTCAGAGGCGAGACCTGT 509

301 GAATATTAACCTCCAGAAATCTACCAAAACGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 360
 510 GAATATTAACCTCCAGAAATCTACCAAAACGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 569
 361 TGCACATGATTAATGATGAGGCGGCGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
 570 TGCACATGATTAATGATGAGGCGGCGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 629
 421 CCCAACTTGGGCTGTCCTCCAAACCTCGGCTGCTGTCCTCAAAAGTTTACGGGCGAGTCTGCGAGAG 480
 630 CCCAACTTGGGCTGTCCTCCAAACCTCGGCTGCTGTCCTCAAAAGTTTACGGGCGAGTCTGCGAGAG 689
 481 TGGGCTCTGAGAGAGATATGATCAAGAGCCCATGAGAGACAGAGAGGCTCTCTTGGC 540
 690 TGGGCTCTGAGAGAGATATGATCAAGAGCCCATGAGAGACAGAGAGGCTCTCTTGGC 749
 541 AAGGAGCTGGGATTTGATGATGCTCTCCGAGTGGAGATTGACAGAAACAAATTAATGATGCA 600
 750 AAGGAGCTGGGATTTGATGATGCTCTCCGAGTGGAGATTGACAGAAACAAATTAATGATGCA 809
 601 GTTGGAAAGGAGGCTCACTGAAGCGGCTCCCTGTTTGGAAATGAGGCTGCAATCTTA 660
 810 GTTGGAAAGGAGGCTCACTGAAGCGGCTCCCTGTTTGGAAATGAGGCTGCAATCTTA 869
 661 TACAACCTTTACAAGGCCAGAAATGATTTGTTCAACAACATTCATGCTCCAGTGTCA 720
 870 TACAACCTTTACAAGGCCAGAAATGATTTGTTCAACAACATTCATGCTCCAGTGTCA 929
 721 AAGACCTGTGAAAGCTGATCTCCACAGAGTTTACCAATGAAACCTGAGCGGCTT 780
 930 AAGACCTGTGAAAGCTGATCTCCACAGAGTTTACCAATGAAACCTGAGCGGCTT 989
 781 GTGAAAGAAACCCGGATTTGTAGAGTGGCGCTTGTGACAGCAGTGTACAGAGCCTG 840
 990 GTGAAAGAAACCCGGATTTGTAGAGTGGCGCTTGTGACAGCAGTGTACAGAGCCTG 1049
 841 AAAAAGGCAAAATATGACAGCAAGCAAGAAATCCCGCAACAGTCAAGTTTACTTAC 900
 1050 AAAAAGGCAAAATATGACAGCAAGCAAGAAATCCCGCAACAGTCAAGTTTACTTAC 1159
 901 GGTGATGTTTGTAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCTGCTGAGAGCGC 960
 1110 GGTGATGTTTGTAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCTGCTGAGAGCGC 1169
 961 CGATGCTGACGCGCCAGCTGACAGAGCTGTGAAGATGCGGTTCCGCTGCAAGATGGG 1020
 1170 CGATGCTGACGCGCCAGCTGACAGAGCTGTGAAGATGCGGTTCCGCTGCAAGATGGG 1229
 1021 GAGACATTTTCCAAAGAGCTCATGATGATCCAGTCTGCAAAATGCACTACAACTGCCCCG 1080
 1230 GAGACATTTTCCAAAGAGCTCATGATGATCCAGTCTGCAAAATGCACTACAACTGCCCCG 1289
 1081 CATGCCAATGAAGAGCGGTTCCCTTCTACAGAGCTGTTCAATGATTCACAAATTTTAAAG 1140
 1290 CATGCCAATGAAGAGCGGTTCCCTTCTTACAGAGCTGTTCAATGATTCACAAATTTTAAAG 1349
 1141 GACTAA 1146
 1350 GACTAA 1355

RESULT 10
 AB088129
 ID AB088129 standard; cDNA; 2021 BP.
 XX
 XX AB088129;
 DT 18-SEP-2002 (first entry)
 XX
 XX Human osteoblast differentiation related cDNA SEQ ID NO 36.
 DE Human; osteoblast; stem cell differentiation; bone tissue deposition;
 KW osteoporosis; osteopath;c; ss.

XX OS Homo sapiens.
XX PN WO200250301-A2.
XX PD 27-JUN-2002.
XX PF 18-DEC-2001; 2001WO-US48276.
XX PR 18-DEC-2000; 2000US-255882P.
XX PR 24-APR-2001; 2001US-285691P.
XX PA (GENE-) GENE LOGIC INC.
XX PA (PROC) PROCTER & GAMBLE CO.
XX PI Ji D, Axelrod DW, Cook JS, Jaiswal N, Einstein R, Houghton A;
XX PI Mertz L;
XX DR WPI; 2002-557663/59.
XX PT Use of genes and their expression profiles associated with osteoblast
XX PT differentiation for screening modulators bone formation, for diagnosing
XX PT or treating e.g. osteoporosis, or as markers for the differentiation
XX PT process
XX PS Claim 1; SEQ ID NO 36; 78bp + Sequence Listing: English.
XX CC The invention relates to genes and their expression profiles are used
XX CC for:
XX CC (a) screening modulators of precursor stem cell differentiation into
XX CC osteoblasts, or bone tissue deposition;
XX CC (b) diagnosing abnormal deposition of bone tissue, abnormal rate of
XX CC osteoblast formation or osteoporosis; or
XX CC (c) treating or monitoring treatment of the conditions cited in (b), or
XX CC monitoring the progression of bone tissue deposition.
XX CC Specific conditions include postmenopausal osteoporosis, glucocorticoid
XX CC osteoporosis or male osteoporosis, osteopenia, osteodystrophy,
XX CC drug-induced abnormalities in bone formation or bone loss, conditions
XX CC that involve altered bone metabolism (e.g. idiopathic juvenile
XX CC osteoporosis), skeletal disease linked to breast cancer, mastocytosis,
XX CC Fanconi Syndrome or fibrous dysplasia. The present sequence is that of an
XX CC osteoblast differentiation associated cDNA marker of the invention.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pcl_sequences.
XX SQ Sequence 2021 BP; 491 A; 529 C; 534 G; 467 T; 0 other;
Query Match 100.0%; Score 1146; DB 24; Length 2021;
Best Local Similarity 100.0%; Pred. No. 8.3e-301;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGCTCCCGCATGCCAGGGGCGCTGCTTGTAGTGTGACCTTCTCCACTTGACGAG 60
DB 215 ATGAGCTCCCGCATGCCAGGGGCGCTGCTTGTAGTGTGACCTTCTCCACTTGACGAG 274
QY 61 CTGGGCGCTTCACCTGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 120
DB 275 CTGGGCGCTTCACCTGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 334
QY 121 CCGGAGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 335 CCGGAGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 394
QY 181 AACGAGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 395 AACGAGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 454
QY 241 GCGGCGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 455 GCGGCGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 514
QY 301 GAATATTAATCTCAGATCTACCAAAACGGGGAAGTTTCCAGCCCACTGTAACATCAG 360

DB 515 GAATATTAATCTCAGATCTACCAAAACGGGGAAGTTTCCAGCCCACTGTAACATCAG 574
QY 361 TGCACATGATATGATGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 575 TGCACATGATATGATGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 634
QY 421 CCCAAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 635 CCCAAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 694
QY 481 TGGGCTGCTGAGAGATAGTATCAAGAGACCCCATGAGAGACAGAGAGAGAGAGAGAGAGAGAG 540
DB 695 TGGGCTGCTGAGAGATAGTATCAAGAGACCCCATGAGAGACAGAGAGAGAGAGAGAGAGAGAG 754
QY 541 AAGGAGCTGGGATTCGATGCTCCGAGAGTGAAGTTCAGAGAAACATGATGATTCGA 600
DB 755 AAGGAGCTGGGATTCGATGCTCCGAGAGTGAAGTTCAGAGAAACATGATGATTCGA 814
QY 601 GTTGAAAGAGGACAGCTGATGAGAGGCTCCCTGTTTGGAAATGAGAGCTCCGATCCTA 660
DB 815 GTTGAAAGAGGACAGCTGATGAGAGGCTCCCTGTTTGGAAATGAGAGCTCCGATCCTA 874
QY 661 TACAACCTTTTACAAGGCGCAGAAATGATGTTTCAACAACACTTCATGCTCCAGTCTCA 720
DB 875 TACAACCTTTTACAAGGCGCAGAAATGATGTTTCAACAACACTTCATGCTCCAGTCTCA 934
QY 721 AAGACCTGTGGAATGCTGATCTCCACAGAGATTCACATGACAAACCTGAGTGGCCTT 780
DB 935 AAGACCTGTGGAATGCTGATCTCCACAGAGATTCACATGACAAACCTGAGTGGCCTT 994
QY 781 GTGAAAGAAACCCGATTTGTGAGTGCGGCTGTGAGACAGCAGATGACAGAGCCTG 840
DB 995 GTGAAAGAAACCCGATTTGTGAGTGCGGCTGTGAGACAGCAGATGACAGAGCCTG 1054
QY 841 AAAAAAGGCAAGAAATGACAGACAGAAAGAAATCCCGAAGCAGTCAAGTTTACTTAC 900
DB 1055 AAAAAAGGCAAGAAATGACAGACAGAAAGAAATCCCGAAGCAGTCAAGTTTACTTAC 1114
QY 901 GCTGATGTTTGAATGATGTAAGAAATACCGGCGCAAGTACTGCTGCTGAGAGCGC 960
DB 1115 GCTGATGTTTGAATGATGTAAGAAATACCGGCGCAAGTACTGCTGCTGAGAGCGC 1174
QY 961 CGATGCTGACAGCGCCAGCTGACAGAGAGCTGGAAGATGCGGTTCCGTGCGTGAAGATGCG 1020
DB 1175 CGATGCTGACAGCGCCAGCTGACAGAGAGCTGGAAGATGCGGTTCCGTGCGTGAAGATGCG 1234
QY 1021 GAGACATTTTCCAGAAAGCTGATGATGATCCAGTCTGCAAAATGCAACTACAGTCCCG 1080
DB 1235 GAGACATTTTCCAGAAAGCTGATGATGATCCAGTCTGCAAAATGCAACTACAGTCCCG 1294
QY 1081 CATGCCAATGAAAGCAGCGTTTCCCTTCTACAGAGCTGTTCAATGACATTCACAAATTTAGG 1140
DB 1295 CATGCCAATGAAAGCAGCGTTTCCCTTCTACAGAGCTGTTCAATGACATTCACAAATTTAGG 1354
QY 1141 GACTAA 1146
DB 1355 GACTAA 1360
RESULT 11
AB088128
ID AB088128 standard; cDNA; 2025 BP.
XX AB088128;
XX AC 18-SEP-2002 (first entry)
XX DT
XX DE Human osteoblast differentiation related cDNA SEQ ID NO 35.
XX XX Human; osteoblast; stem cell differentiation; bone tissue deposition;
XX KW osteoporosis; osteopathic; ss.
XX

OS Homo sapiens.
 PN MO200250301-A2.
 XX 27-JUN-2002.
 PD
 XX
 PF 18-DEC-2001; 2001WO-US48276.
 XX
 XX 18-DEC-2000; 2000US-255882P.
 PR 24-APR-2001; 2001US-285691P.
 XX
 PA (GENE-) GENE LOGIC INC.
 PA (PROCTER & GAMBLE CO.
 PI J1 D, Axelrod DW, Cook JS, Jaiswal N, Einstein R, Houghton A;
 PI Mertz L;
 DR WPI; 2002-557663/59.
 XX
 PT Use of genes and their expression profiles associated with osteoblast
 PT differentiation for screening modulators bone formation, for diagnosing
 PT or treating e.g. osteoporosis, or as markers for the differentiation
 PT process -
 PS
 PS Claim 1; SEQ ID NO 35; 78bp + Sequence Listing; English.
 CC
 CC The invention relates to genes and their expression profiles are used
 CC for:
 CC (a) screening modulators of precursor stem cell differentiation into
 CC osteoblasts, or bone tissue deposition;
 CC (b) diagnosing abnormal deposition of bone tissue, abnormal rate of
 CC osteoblast formation or osteoporosis; or
 CC (c) treating or monitoring treatment of the conditions cited in (b), or
 CC monitoring the progression of bone tissue deposition.
 CC Specific conditions include postmenopausal osteoporosis, glucocorticoid
 CC osteoporosis or male osteoporosis, osteopenia, osteodystrophy,
 CC drug-induced abnormalities in bone formation or bone loss, conditions
 CC that involve altered bone metabolism (e.g. idiopathic juvenile
 CC osteoporosis), skeletal disease linked to breast cancer, mastocytosis,
 CC Fanconi syndrome or fibrous dysplasia. The present sequence is that of an
 CC osteoblast differentiation associated cDNA marker of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 CC
 CC
 SQ Sequence 2025 BP; 490 A; 531 C; 537 G; 467 T; 0 other;
 Query Match 100.0%; Score 1146; DB 24; Length 2025;
 Best local Similarity 100.0%; Pred. No. 8.3e-301;
 Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 519 GAATATTAAGTCCAGAAATCTACCAAAAGGGGAAAGTTTCCAGCCCACTGTAAATCATAG 578
 Qy
 Db 361 TGCACATGATATGATGGCCCGGTGGCGTCATCTCTGTGTGCCCAAGAACTATCTCTC 420
 Qy
 Db 579 TGCACATGATATGATGGCCCGGTGGCGTCATCTCTGTGTGCCCAAGAACTATCTCTC 638
 Qy
 Db 421 CCCAAGTTGGGCTGTCCCAACCCCTGGCTGTCTCAAGTTACCGGGGCAATGCTGCGAGAG 480
 Qy
 Db 639 CCCAAGTTGGGCTGTCCCAACCCCTGGCTGTCTCAAGTTACCGGGGCAATGCTGCGAGAG 698
 Qy
 Db 481 TGGGCTGTGAGAGATGATATCAAGAGACCCCATGAGAGACGAGGAGGCGCTGCTGGC 540
 Qy
 Db 699 TGGGCTGTGAGAGATGATATCAAGAGACCCCATGAGAGACGAGGAGGCGCTGCTGGC 758
 Qy
 Db 541 AAGGAGCTGGAGATTCATGCTCCAGAGTGAAGTTGACGAGAAACATGAATGATGGA 600
 Db 759 AAGGAGCTGGAGATTCATGCTCCAGAGTGAAGTTGACGAGAAACATGAATGATGGA 818
 Qy
 Db 601 GTTGGAAAAGGACGCTCATGAAAGCGGCTCCCTGTTTGGAAATGAGAGCTGCAATCTTA 660
 Db 819 GTTGGAAAAGGACGCTCATGAAAGCGGCTCCCTGTTTGGAAATGAGAGCTGCAATCTTA 878
 Qy
 Db 661 TACAACTTTTCAAGAGCCAGAAATGATTTTCAACAACCTTCATGCTCCAGTGTCTCA 720
 Db 879 TACAACTTTTCAAGAGCCAGAAATGATTTTCAACAACCTTCATGCTCCAGTGTCTCA 938
 Qy
 Db 721 AAGACCTGTGAAGTGTATCTCCACAGAGTTTACCAATGACAAACCTGATGCGCCCTT 780
 Db 939 AAGACCTGTGAAGTGTATCTCCACAGAGTTTACCAATGACAAACCTGATGCGCCCTT 998
 Qy
 Db 781 GTGAAAAGAACCCGGATTTGTGAGTGGCGCTTGTGAGACAGCAATGATGACAGCCTG 840
 Db 999 GTGAAAAGAACCCGGATTTGTGAGTGGCGCTTGTGAGACAGCAATGATGACAGCCTG 1058
 Qy
 Db 841 AAAAAGGGAAGAAATGACGAAAGACCAAGAAATCCCGAAGCACTGAGTTTACTTAC 900
 Db 1059 AAAAAGGGAAGAAATGACGAAAGACCAAGAAATCCCGAAGCACTGAGTTTACTTAC 1118
 Qy
 Db 901 GCTGATGTTTGTAGTGTGAAGAAATACGCGCCCAAGTACTGCGGTTCTGCTGACGCG 960
 Db 1119 GCTGATGTTTGTAGTGTGAAGAAATACGCGCCCAAGTACTGCGGTTCTGCTGACGCG 1178
 Qy
 Db 961 CGATGCTGACCGCCAGCTGACAGCAAGTGTGAATCGGTTCCGTCGCAAGATGGG 1020
 Db 1179 CGATGCTGACCGCCAGCTGACAGCAAGTGTGAATCGGTTCCGTCGCAAGATGGG 1238
 Qy
 Db 1021 GAGACATTTTCCAGAAAGCTCATGATGATCCAGTCTGCAAAATGCAACTAACTGCCG 1080
 Db 1239 GAGACATTTTCCAGAAAGCTCATGATGATCCAGTCTGCAAAATGCAACTAACTGCCG 1298
 Qy
 Db 1081 CATGCCAATGAAGACAGCGTTTCCCTTCTAAGGCTGTTCATGACATTCACAAATTTAG 1140
 Qy
 Db 1299 CATGCCAATGAAGACAGCGTTTCCCTTCTAAGGCTGTTCATGACATTCACAAATTTAG 1358
 Qy
 Db 1141 GACTAA 1146
 Db 1359 GACTAA 1364

RESULT 12
 AAC78196
 ID AAC78196 standard; cDNA; 2307 BP.
 XX
 AC AAC78196;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Human cancer associated gene sequence SEQ ID NO:590.
 XX
 XX Human: cancer associated gene; cancer antigen; detection; cancer;
 KW diagnosis; cytostatic; proliferative; vulnerable; immunomodulatory;
 KW antidiabetic; antihistaminic; antineuritic; antitachycardic; antitumor;
 KW antiinflammatory; antihypertensive; antibacterial; cardiac;

KW dermatological; neuroprotective; thrombolytic; coagulant; nootropic;
 KW vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
 KW immune disorder; haematopoietic cell disorder; autoimmune disorder;
 KW allergic reaction; graft versus host disease; organ rejection;
 KW haemostatic; thrombolytic; cardiovascular disorder; infection;
 KW neurological disease; drug screening; ss.
 XX Homo sapiens.
 OS
 PN M0200055350-A1.
 PD 21-SEP-2000.
 PF 08-MAR-2000; 2000MO-US05882.
 PR 12-MAR-1999; 99US-0124270.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Rosen CA, Ruben SM;
 PI
 XX MPI: 2000-587533/55.
 DR P-PSDB: AAB43987.
 PT Novel isolated nucleic acids comprising sequences encoding peptides
 useful for treating or diagnosing e.g. cancer -
 PS
 XX Claim 1: Page 1112; 2352pp; English.
 CC AAC7607 to AAC78448 encode the human cancer associated proteins given
 CC in AAB4398 to AAB44233. The proteins can have activities based on the
 CC tissues and cells the genes are expressed in. Example of activities
 CC include: cytostatic; proliferative; vulnerary; immunomodulator;
 CC antidiabetic; antisthmatic; antirheumatic; antitarrhetic;
 CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
 CC dermatologic; neuroprotective; cardiac; thrombolytic; coagulant;
 CC nootropic; vasotropic; antipsoriatic and antiangiogenic. The
 CC polynucleotides and polypeptides can be used for preventing, treating or
 CC ameliorating medical conditions and diagnosing pathological conditions.
 CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from
 CC the present invention may be used to treat immune disorders by activating
 CC or inhibiting the proliferation, differentiation or mobilisation of
 CC immune cells, to treat disorders of haematopoietic cells, autoimmune
 CC disorders, allergic reactions, graft versus host disease and organ
 CC rejection, modulate haemostatic or thrombolytic activity, modulate
 CC inflammation, cancers, cardiovascular disorders, neurological disease and
 CC bacterial or viral infections. The peptides, nucleotides, antibodies,
 CC agonists and antagonists may be also be used in drug screens. AAC78449 to
 CC AAC78457 and AAB44240 represent sequences used in the exemplification of
 CC the present invention.
 CC
 XX
 SO Sequence 2307 BP; 610 A; 573 C; 580 G; 544 T; 0 other;

Query Match 100.0%; Score 1146; DB 21; Length 2307;
 Best Local Similarity 100.0%; Pred. No. 8,8e-301;
 Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 241 GGGCCACGCTCCACCGCTCTGAAAGGGATGTGACAGCTGACGACGAGCCCTGT 300
 |||||||
 Db 463 GGGCCACGCTCCACCGCTCTGAAAGGGATGTGACAGCTGACGACGAGCCCTGT 522
 QY 301 GAATATATACCTCCAGATCTACCAAAACGGGAAAATTCCAGCCCACTGTAACATCAG 360
 |||||||
 Db 523 GAATATATACCTCCAGATCTACCAAAACGGGAAAATTCCAGCCCACTGTAACATCAG 582
 QY 361 TGCACATGTATGTGATGGCGCGTGGGCTGATTCCTCTGTGTCGCCCAAGAAATATCTCTC 420
 |||||||
 Db 583 TGCACATGTATGTGATGGCGCGTGGGCTGATTCCTCTGTGTCGCCCAAGAAATATCTCTC 642
 QY 421 CCCAATCTGGGCTGTCCCAACCCCTCGCTGCTCAAAAGTTACCGGGCAGTCTCGGAGAG 480
 |||||||
 Db 643 CCCAATCTGGGCTGTCCCAACCCCTCGCTGCTCAAAAGTTACCGGGCAGTCTCGGAGAG 702
 QY 481 TGGGCTGTGACGAGATAGTATCAGAGACCCCATGAGACACGAGCGCTCTCTGGC 540
 |||||||
 Db 703 TGGGCTGTGACGAGATAGTATCAGAGACCCCATGAGACACGAGCGCTCTCTGGC 762
 QY 541 AAGGAGCTGGGATTCGATGCTCCGAGGTGAGAGTTCAGAAACATGATGATGCA 600
 |||||||
 Db 763 AAGGAGCTGGGATTCGATGCTCCGAGGTGAGAGTTCAGAAACATGATGATGCA 822
 QY 601 GTTGAAAAAGGACAGCTACTGTAAGCGGCTCCCTGTTTGGATGAGAGCTCGCATCTTA 660
 |||||||
 Db 823 GTTGAAAAAGGACAGCTACTGTAAGCGGCTCCCTGTTTGGATGAGAGCTCGCATCTTA 882
 QY 661 TACAACCTTTTACAAAGCCAGAAATGATTTGTTCAAAACACTTCATGATGATGCA 720
 |||||||
 Db 883 TACAACCTTTTACAAAGCCAGAAATGATTTGTTCAAAACACTTCATGATGATGCA 942
 QY 721 AAGACCTGTGAACTGTATCTCCACAGAGTTCACAAATGCAACCTGAGTGGCGCTT 780
 |||||||
 Db 943 AAGACCTGTGAACTGTATCTCCACAGAGTTCACAAATGCAACCTGAGTGGCGCTT 1002
 QY 781 GTGAAAGAAACCCGATTTGTGAGGTGCGGCTTGTGAGACAGCAGTACAGAGCCTG 840
 |||||||
 Db 1003 GTGAAAGAAACCCGATTTGTGAGGTGCGGCTTGTGAGACAGCAGTACAGAGCCTG 1062
 QY 841 AAAAAAGGCAAGAAATGACAGCAGACCAAGAAATCCCGCAACAGTACAGTTCATTAC 900
 |||||||
 Db 1063 AAAAAAGGCAAGAAATGACAGCAGACCAAGAAATCCCGCAACAGTACAGTTCATTAC 1122
 QY 901 GCTGATGTTGATGATGAAATACCGGCGCAAGTACGCGGTTCTGCTGAGAGCGC 960
 |||||||
 Db 1123 GCTGATGTTGATGATGAAATACCGGCGCAAGTACGCGGTTCTGCTGAGAGCGC 1182
 QY 961 CGATGCTGACAGCCCGACGCTGACAGGACTGTGAAGATGCGGTTCCGCTGGAAGATGG 1020
 |||||||
 Db 1183 CGATGCTGACAGCCCGACGCTGACAGGACTGTGAAGATGCGGTTCCGCTGGAAGATGG 1242
 QY 1021 GAGACATTTTCCAAAGACGTATGATATCCAGTCTGCAAAATGCAACTACACTGCCCG 1080
 |||||||
 Db 1243 GAGACATTTTCCAAAGACGTATGATATCCAGTCTGCAAAATGCAACTACACTGCCCG 1302
 QY 1081 CATGCCAATGAAGAGGTTTCCCTCTACAGGTTGTTCAATGATTCATCAAAATTTAGG 1140
 |||||||
 Db 1303 CATGCCAATGAAGAGGTTTCCCTCTACAGGTTGTTCAATGATTCATCAAAATTTAGG 1362
 QY 1141 GACTTAA 1146
 |||||||
 Db 1363 GACTTAA 1368

RESULT 13
 AB08127
 ID AB08127 standard; cdna; 2052 BP.
 XX
 XX AB08127;
 DT 18-SEP-2002 (first entry)
 XX

DE Human osteoblast differentiation related cDNA SEQ ID NO 34.
 XX Human; osteoblast; stem cell differentiation; bone tissue deposition;
 KW osteoporosis; osteopathic; ss.
 XX Homo sapiens.
 OS
 PN MO200250301-A2.
 PD 27-JUN-2002.
 XX
 PF 18-DEC-2001; 2001MO-US48276.
 XX
 PR 18-DEC-2000; 2000US-25582P.
 PR 24-APR-2001; 2001US-285691P.
 XX
 PA (GENE-) GENE LOGIC INC.
 PA (PROC) PROCTER & GAMBLE CO.
 XX
 PI JI D, Axelrod DW, Cook JS, Jaiswal N, Einstein R, Houghton A;
 PI Mertz L;
 DR MPI; 2002-557663/59.
 XX
 PT Use of genes and their expression profiles associated with osteoblast
 PT differentiation for screening modulators bone formation, for diagnosing
 PT or treating e.g. osteoporosis, or as markers for the differentiation
 PT process
 XX
 PS Claim 1; SEQ ID NO 34; 78bp + Sequence Listing; English.
 XX
 CC The invention relates to genes and their expression profiles are used
 CC for:
 CC (a) screening modulators of precursor stem cell differentiation into
 CC osteoblasts, or bone tissue deposition;
 CC (b) diagnosing abnormal deposition of bone tissue, abnormal rate of
 CC osteoblast formation or osteoporosis; or
 CC (c) treating or monitoring treatment of the conditions cited in (b), or
 CC monitoring the progression of bone tissue deposition.
 CC Specific conditions include postmenopausal osteoporosis, glucocorticoid
 CC osteoporosis or male osteoporosis, osteopenia, osteodystrophy,
 CC drug-induced abnormalities in bone formation or bone loss, conditions
 CC that involve altered bone metabolism (e.g. idiopathic juvenile
 CC osteoporosis), skeletal disease linked to breast cancer, mastocytosis,
 CC Fanconi syndrome or fibrous dysplasia. The present sequence is that of an
 CC osteoblast differentiation associated cDNA marker of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 2052 BP; 499 A; 542 C; 543 G; 468 T; 0 other;

Query Match 99.9%; Score 1144.4; DB 24; Length 2052;
 Best Local Similarity 99.9%; Pred. No. 2.3e-300;
 Matches 1145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAGTCCCGCAGTCCGAGGCGCTGCTTGTAGTGTACCTTGTGACCTTGTGACCAAG 60
 DB ATGAGTCCCGCAGTCCGAGGCGCTGCTTGTAGTGTACCTTGTGACCTTGTGACCAAG 283
 QY 61 CTGGGCGCTGCTGCACTGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
 DB CTGGGCGCTGCTGCACTGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 343
 QY 121 CCGGAGTGGGCTGCTGCGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
 DB CCGGAGTGGGCTGCTGCGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 403
 QY 181 AACGAGTGTGAGCAAAAGCAGCCCTGCGACACACCAAGGCGCTGGAATGCAACTTC 240
 DB AACGAGTGTGAGCAAAAGCAGCCCTGCGACACACCAAGGCGCTGGAATGCAACTTC 463
 QY 241 GCGCGCAGCTCCACCGCTGTGAAGGGGAGTGTGAGAGCTCAGTCAAGAGGCGACACCTGT 300

DB 464 GCGCGCAGCTCCACCGCTGTGAAGGGGATCTGAGAGCTCAGTCAAGAGGCGACACCTGT 523
 QY 301 GAATATACCTCCAGATCTACCAAAAGGGGAAATTTCCAGCCCAAGTGAATCAATCAG 360
 DB 524 GAATATACCTCCAGATCTACCAAAAGGGGAAATTTCCAGCCCAAGTGAATCAATCAG 583
 QY 361 TGCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
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 QY 421 CCCAATTTGGGCTGTCCCAACCTCGGCTGTGTAAAGTTACCGGGGAGTGTGTGTGAG 480
 DB CCCAATTTGGGCTGTCCCAACCTCGGCTGTGTAAAGTTACCGGGGAGTGTGTGTGAG 703
 QY 481 TGGGTCTGTGACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 DB TGGGTCTGTGACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 763
 QY 541 AAGGAGCTGGGATTCGATGCTCCGAGGTGAGTGTGACGAGAAATGATGATGATGATGAT 600
 DB AAGGAGCTGGGATTCGATGCTCCGAGGTGAGTGTGACGAGAAATGATGATGATGATGAT 823
 QY 601 GTTGAAGAGGCGCTCAGTGAAGGGCTCCCTGTTTGGAAATGAGGCTGCAATCTCA 660
 DB GTTGAAGAGGCGCTCAGTGAAGGGCTCCCTGTTTGGAAATGAGGCTGCAATCTCA 883
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 DB GTTGAAGAGGCGCTCAGTGAAGGGCTCCCTGTTTGGAAATGAGGCTGCAATCTCA 943
 QY 884 TACACCTTTTACAAAGGCGAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 943
 DB TACACCTTTTACAAAGGCGAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 1003
 QY 944 AAGACCTGTGGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1003
 DB AAGACCTGTGGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1063
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 DB GTGAAAGAAACCGGATTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1123
 QY 841 AAAAAGGCGAGAAATGACAGCAAGACCAAGAAATCCCGAAGCACTGAGTTTACTTAC 900
 DB AAAAAGGCGAGAAATGACAGCAAGACCAAGAAATCCCGAAGCACTGAGTTTACTTAC 1123
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 QY 901 GCTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
 DB GCTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1183
 QY 1124 GCTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1183
 DB GCTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1243
 QY 961 CGATGCTGACGCGCCGAGCTGACACGAGCTGTGAAGATGCGGTTCCGTCGGAAGTGGG 1020
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 QY 1304 CATGCCAATGAAGACGCTTTCCCTTCTACAGGCTTTTCAATGACATTCACAAATTTAG 1363
 DB CATGCCAATGAAGACGCTTTCCCTTCTACAGGCTTTTCAATGACATTCACAAATTTAG 1446
 QY 1141 GACTAA 1146
 DB 1364 GACTAA 1369

RESULT 14
 AAT94699 standard; cDNA: 1418 BP.
 ID AAT94699
 XX AAT94699;
 AC AAT94699;
 XX
 DT 27-MAR-1998 (first entry)
 XX
 DE Human cysteine rich protein 61 (Cyr61) cDNA.

XX	Cysteine rich protein 61; Cyr61; human;
KW	extracellular matrix signalling molecule; cell adhesion;
RK	cell migration; cell proliferation; angiogenesis; chondrogenesis;
KV	oncogenes; haemostasis; wound healing; organ regeneration; ss.
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	124..1269
CD	/tag= a
XX	
PN	M09733995-A2.
XX	
PD	18-SEP-1997.
XX	
PE	14-MAR-1997; 97WO-US04193.
XX	
PR	15-MAR-1996; 96US-0013958.
XX	
PA	(MUNI-) MUNIN CORP.
XX	
Lau LF:	
PI	
DR	WP1: 1997-470875/43.
P-PDB:	AAM35730.
XX	
PT	Isolated and purified cysteine rich protein 61, Cyr61 - useful to modulate e.g. haematocytosis, induce wound healing, promote organ regeneration etc
PS	Claim 14; Page 110-112; 13pp; English.
XX	
CC	This cDNA clone codes for human cysteine rich protein 61 (Cyr61) (see AAM35760), an extracellular matrix signalling molecule. It was isolated from a human placental CDNA library using as probe a partial clone obtained by PCR amplification using primers (see AAT94701-02) based on conserved regions of murine Cyr61. Cyr61 polynucleotides can be used for the production of murine Cyr61 recombinant methods and as hybridisation probes. Cyr61 can be used to modulate haematocytosis, induce wound healing in a tissue, promote organ regeneration, improve tissue grafting or promote bone or prosthesis implantation (claimed). It can also be used to screen for a modulator of angiogenesis, chondrogenesis, oncogenesis, cell adhesion, cell migration, cell proliferation, expand a population of undifferentiated haematopoietic stem cells in culture and to screen for a mitogen (claimed). Knowledge of the Cyr61 coding sequence provides the basis for the design of gene therapy approaches.
CC	
CC	
SQ	Sequence 1418 BP; 334 A; 407 C; 398 G; 279 T; 0 other;
OQuery Match	99.7%; Score 1142.8; DB 18; Length 1418;
Bst Local Similarity	99.8%; Pred. No.5.2e-300; Indels 0; Gaps 0;
Matches 1144;	Conservative 0; Mismatches 2;
OY	1 ATGAGCTCCCACATCGCCAGGGGCGGTGCCTTAA GTCATGCCCTTCCTCACTTGACAAG 60 Db 124 ATGAGCTCCGCATATGCCAAGGGGCGGTGCCTTA AGTCATCACCTTCCTCACTTGACAAG 183 OY 61 CTGGGCGCTCTCCACTCGCCCGCGTTGCGCACTGCCCCCTTGAGA GGCGCCAATTGCGG 120 Db 184 TTGGGGCTCTCTACCCTTGCCTCCGCTGCACTGCCTCCCTTGGAAGGCCCCCAA GTGGCG 243 OY 121 CGGGGAGTCGGGGCTGTGCGGGAGCGCTGCGGCTGCTTAAGAGCTTGCGCCAAGCAAGCTC 180 Db 244 CCGGGAGTCGGGGCTGTGCTCGGGAGCGGTGCGGCTGCTTAAGCTTGCGCCAAGCAAGCTC 303 OY 181 AACGAGACTCTCAGCAAAAACGACGCTGCGAACACACCAAGGGGCTGGAA TGCAACTTC 240 Db 304 AACGAGACTCTCAGCAAAAAACGACGCTGCGAACACACCAAGGGGCTGGAA TGCAACTTC 363 OY 241 GGCGCCACTCCACCGCTCTGTGAAGGGGATCTTGACAGAGCTCACTCA GAAGGGCAGACCTGT 300

Dd		364	GGCGCAGCTCCACGCGCTGTGAAGGGATTCGCAAGTCTAGTAGAGGCCAGCCTTGT	423
Oy		301	GAAATATACTCCAAATCTACCAAAGGGGAAAATTCCAGCCCCAATGTAAACTAG	360
Dd		424	GAATTAATCTCCAAATCTACCBAAGGGGAAAGTTCCAGCCCMACTGTCAACATCAG	483
Oy		361	TGCACATGATTTGATGGGCGCGTGCGCTGCATTCCTCTGTGTGCCAAGAATCATCTCTC	420
Dd		484	TGCACATGATTTGATGGGCGCGTGCGCTGCATTCCTCTGTGTGCCAAGAATCATCTCTC	543
Oy		421	CCCAACTTGGGCTGTCCCAACCCCTGGCTGGTCAAAGTTACGGGGCAGTGTGGAGAG	480
Dd		544	CCCAACTTGGGCTGTCCCAACCCCTGGCTGGTCAAAGTTACCGGGCAGTGTGGAGAG	603
Oy		481	TGGGCTGTGACGAGATAGTATCAAGAACCCCATGGAGACCAAGAGCGGCTCCTTGGC	540
Dd		604	TGGGCTGTGACGAGATAGTATCAAGAACCCCATGGAGACCAAGAGCGGCTCCTTGGC	663
Oy		541	AAGAGCTGGGATTCGATCGCTCCGAGGTGAGTTGACGAGAAACAATGAATTGATGCA	600
Dd		664	AAGAGCTGGGATTCGATCGCTCCGAGGTGAGTTGACGAGAAACAATGAATTGATGCA	723
Oy		601	GTTGGAAAGGCAGCTCAGTAAGCGGCTCCCTGTTTTGGAATGAGAGCTCGATCCTA	660
Dd		724	GTTGGAAAGGCAGCTCAGTAAGCGGCTCCCTGTTTTGGAATGAGAGCGCTCGATCCTA	783
Oy		661	TACAAACCTTTACAAAGGCCAGAAAATGTTATTTTAAACAACTTATAGTCCAGTGTCA	720
Dd		784	TACAAACCTTTACAAAGGCCAGAAAATGTTATTTTAAACAACTTATAGTCCAGTGTCA	843
Oy		721	AAGACCTGTGAGACTGTATCTCCACACGAGTTACCAATGCAACACCTGATGGCGCTT	780
Dd		844	AAGACCTGTGAGACTGTATCTCCACACGAGTTACCAATGCAACACCTGATGGCGCTT	903
Oy		781	GTGAAAGAAACCCGGATTTGTGAGGTGGGCGCTGTGACAGCCAGTGTACGACGCTG	840
Dd		904	GTGAAAGAAACCCGGATTTGTGAGGTGGGCGCTGTGACAGCCAGTGTACGACGCTG	963
Oy		841	AAAAAGGSCAAGAAATGACGACAAGCAAGAATAATCCCGCAACAGTCAGSTTACTTAC	900
Dd		964	AAAAAGGSCAAGAAATGACGACAAGCAAGAATAATCCCGCAACAGTCAGSTTACTTAC	1023
Oy		901	GCTGGATGTTGATGTGTAAGAAATACCGGCCCAAGTACTCGGGTTCCTGCGTGGACGGC	960
Dd		1024	GCTGGATGTTGATGTGTAAGAAATACCGGCCCAAGTACTCGGGTTCCTGCGTGGACGGC	1083
Oy		961	CGATGCTCACGCCCCAGCTACCAAGACTGTGAAGATGCGGTTCCGTGCGAAGATGGG	1020
Dd		1084	CGATGCTCACGCCCCAGCTACCAAGACTGTGAAGATGCGGTTCCGTGCGAAGATGGG	1143
Oy		1021	GAGCAATTTTCCAAGAACGTGATGATGATCAGTCCCTCAAAATGGAATACACTGCGCCG	1080
Dd		1144	GAGCAATTTTCCAAGAACGTGATGATGATCAGTCCCTCAAAATGGAATACACTGCGCCG	1203
Oy		1081	CATGCCAATGAAGAGCGTTTCCCTTCTACAGGCGTGTCAATGACATTCACAAATTAGG	1140
Dd		1204	CATGCCAATGAAGAGCGTTTCCCTTCTACAGGCGTGTCAATGACATTCACAAATTAGG	1263
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Dd		1264	GACTRA 1269	
<hr/>				
RESULT 15				
AAD11221 standard; cDNA; 1418 BP.				
xx	AAD11221;			
xx	AAD11221;			
xx	24-Sep-2001	(first entry)		
DE	Human cysteine-rich protein (Cyr61) cDNA.			

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 10, 2003, 06:16:29 ; Search time 1897 Seconds
(without alignments)
9783.884 Million cell updates/sec

Title: US-09-901-910-1

Perfect score: 1146
Sequence: 1 atgagctccgcgcacgcacg.....ttcaccaatttaggactaa 1146

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	894.4	78.0	2029	11	BC003205 mus muscu
2	876.8	76.5	919	14	BQ925203 AGENCOURT
3	807.6	70.5	895	14	BQ880408 AGENCOURT
4	797.6	69.6	866	14	BQ222696 AGENCOURT
5	769.6	67.2	939	14	BQ644239 AGENCOURT
6	762.4	66.5	985	9	AL550072 AL550072

Result No.	Score	Query Match	Length	DB ID	Description
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8	751.6	65.6	992	14	BQ644666 AGENCOURT
9	749.8	65.4	888	12	BQ698245 AGENCOURT
10	748.8	65.3	1009	9	AL513570 AL513570
11	746	65.1	836	14	BQ716992 AGENCOURT
12	738.6	64.5	908	14	BQ720988 AGENCOURT
13	726	63.4	896	14	BQ719732 AGENCOURT
14	722.6	63.1	929	9	AL541592 AL541592
15	714	62.3	1083	13	BM479014 AGENCOURT
16	700.2	61.1	935	9	AL545099 AL545099
17	700.2	61.1	943	9	AL553324 AL553324
18	695	60.6	912	9	AL542382 AL542382
19	682.2	59.5	982	9	AL550752 AL550752
20	681	59.4	831	12	BE742330 AGENCOURT
21	676.2	59.0	826	12	BG116760 AGENCOURT
22	667.2	58.2	912	12	BG117213 AGENCOURT
23	661.8	57.7	951	9	AL549837 AL549837
24	654.2	57.1	942	9	AL544453 AL544453
25	648	56.5	879	12	BG163309 AGENCOURT
26	644.4	56.2	877	9	AL546864 AL546864
27	633.2	55.3	927	13	BH16801 AGENCOURT
28	633	55.2	927	12	BE792754 AGENCOURT
29	629.4	54.9	955	14	BQ900935 AGENCOURT
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31	627.6	54.8	822	12	BG122198 AGENCOURT
32	625.4	54.6	828	9	AL543019 AL543019
33	623.6	54.4	921	14	BQ706487 AGENCOURT
34	622	54.3	758	12	BG327746 AGENCOURT
35	617	53.8	879	12	BE747258 AGENCOURT
36	617	53.8	880	12	BE740544 AGENCOURT
37	610	53.2	720	13	BH089906 AGENCOURT
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39	597.4	52.1	888	9	AL544380 AL544380
40	596.8	52.1	812	12	BE880073 AGENCOURT
41	593.6	51.8	611	10	AM580842 AGENCOURT
42	593.4	51.8	641	10	AM580835 AGENCOURT
43	592	51.7	628	10	AM580963 AGENCOURT
44	588.4	51.3	1004	13	BM472832 AGENCOURT
45	587.6	51.3	613	10	AM580928 AGENCOURT

ALIGNMENTS

RESULT 1
BC003205
LOCUS
DEFINITION Mus musculus, cysteine rich protein 61, clone IMAGE:3587352, mRNA.
ACCESSION BC003205
VERSION BC003205.1 GI:14707674
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2029)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgaps-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNI)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu


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/lab_host="DH10B"
/Note="Vector: PCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCAGCGCTCG-3' and
5'-GACTAGTTCTAGATGCGAGCGGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."

BASE COUNT      241 a      238 c      244 g      196 t
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Query Match      76.5%; Score 876.8; DB 14; Length 919;
Best Local Similarity 99.0%; Pred. No. 2,1e-232;
Matches 903; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

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Db 1 AACTTCGGCGCCAGCTCCACCGCTCTGAGGGGATCTGACAGCTCAGTCAAGAGCGAGA 60
QY 295 CCCTGTGAATTAATCTCCAGATCTACCAAAACGGGGAAAGTTTCCAGCCCACTGTAAA 354
    |||||||
Db 61 CCCTGTGAATTAATCTCCAGATCTACCAAAACGGGGAAAGTTTCCAGCCCACTGTAAA 120
QY 355 CATCAGTGCATATGATGATGGGGCGGTGGCGTCATTCCTCTGTGTCCTCCCAAGACTA 414
    |||||||
Db 121 CATCAGTGCATATGATGATGGGGCGGTGGCGTCATTCCTCTGTGTCCTCCCAAGACTA 180
QY 415 TCTCTCCCAACTTGGGCTGTCCCAACCTCTGCGTGGTCAAGTTACCGGGCACTGTGC 474
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Db 181 TCTCTCCCAACTTGGGCTGTCCCAACCTCTGCGTGGTCAAGTTACCGGGCACTGTGC 240
QY 475 GAGGAGTGGGTCTGTGACGAGATGATATCAAGAGACCCCATGAGAGACGAGCGCTC 534
    |||||||
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QY 535 CTTGGCAAGGAGCTGGGATTCGATCGATCCGAGGTGAGTTCAGAGAAACAAATGATG 594
    |||||||
Db 301 CTTGGCAAGGAGCTGGGATTCGATCGATCCGAGGTGAGTTCAGAGAAACAAATGATG 360
QY 595 ATTCAGATGGAAAAAGGAGCTCACTGAGCGGCTCCCTGTTTGGATGAGCTCTGC 654
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Db 361 ATTCAGATGGAAAAAGGAGCTCACTGAGCGGCTCCCTGTTTGGATGAGCTCTGC 420
QY 655 ATTCATATCAACCTTTACAAGGCCAGAAATGTAATGTCAAACACTTCATGTCCTCAG 714
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Db 421 ATTCATATCAACCTTTACAAGGCCAGAAATGTAATGTCAAACACTTCATGTCCTCAG 480
QY 715 TGCCTCAAAAGCTGTGAGTCTATCTCCACAGAGTACCATGACACCCGAGTGC 774
    |||||||
Db 481 TGCCTCAAAAGCTGTGAGTCTATCTCCACAGAGTACCATGACACCCGAGTGC 540
QY 775 CGCCTTGTGAAGAAACCCGATTTGTGAGGTGGCGCTTGTGACACAGCTGATACAGC 834
    |||||||
Db 541 CGCCTTGTGAAGAAACCCGATTTGTGAGGTGGCGCTTGTGACACAGCTGATACAGC 600
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Db 601 AGCCTGAAAAAGGCGCAAGAAATGACAGCAAGCAAGAAATCCCCGAAACAGTCAAGTTT 660
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    |||||||
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QY 955 GAGGCGGATGCTCAGCGCCAGCTGACAGAGCTGGAAGATGCGGTTCCGCTGCGAA 1014
    |||||||
Db 721 GAGGCGGATGCTCAGCGCCAGCTGACAGAGCTGGAAGATGCGGTTCCGCTGCGAA 780
QY 1015 GATGGGGAGACATTTTCCAAAGACGTCATGATTCACGATCTCGAAATGCAACTACAAAC 1074
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Db 781 GATGGGGAGA-ATTTTCCAAAGACATCATGATATCCAGCTCTGCAATGCAACTAC-AC 838
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Db 839 TGCCCGCATGCATGAGAGAGGCTTCCCTTACAGGGCTTCAATGACATTCACAAA 898
QY 1135 TTTAGGACTTAA 1146
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RESULT 3
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DEFINITION
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ACCESSION
BO880408
VERSION
BO880408.1 GI:22272416
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 895)
AUTHORS
NIH-MGC http://mgc.ncl.nih.gov/
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: ggapbs-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Agencourt Bioscience Corporation
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLMJ3565 row: 1 column: 24
High quality sequence stop: 660.
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Location/Qualifiers
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/Note="Vector: PCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCAGCGCTCG-3' and
5'-GACTAGTTCTAGATGCGAGCGGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."

BASE COUNT      229 a      236 c      251 g      179 t
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Query Match      70.5%; Score 807.6; DB 14; Length 895;
Best Local Similarity 97.8%; Pred. No. 3,6e-213;
Matches 851; Conservative 0; Mismatches 14; Indels 5; Gaps 3;

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Db 1 GCTGTCCGGGAGCGCTGCGCTCTGTAAGCTTGCGCCAAAGAGCTCAAGAGAGCTG 60
QY 192 CAGCAAAAACGAGCCCTGCGACACACCAAGGGCTGGAATGCAATTCGGCGCCACTC 251
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Db 61 CAGCAAAAACGAGCCCTGCGACACACCAAGGGCTGGAATGCAATTCGGCGCCACTC 120

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QY 252 CACCGCTCTGAAAGGGATCTGCAGAGCTAGTCAGAGGGCAGCCCTGTGAAATATTAATC 311
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QY 372 TGAATGGCGCGTGGGCTGCATTCCTGTGTCTCCCAAGAACTATCTCTCCCACTTGGG 431
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Db 241 TGAATGGCGCGTGGGCTGCATTCCTGTGTCTCCCAAGAACTATCTCTCCCACTTGGG 300
QY 432 CTGTCCCAACCTCGCTGTGTCAAGTTACCGGGCAGTGTGCGAGAGTGGTGTGTA 491
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Db 301 CTGTCCCAACCTCGCTGTGTCAAGTTACCGGGCAGTGTGCGAGAGTGGTGTGTA 360
QY 492 CGAGATAGTATCAAGAGCCCATGAGAGCCAGAGCGGCTCTTGGCAAGAGAGTGGG 551
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QY 732 AACTGTATCTCCACAGAGTTACCAATGACAACCTGAGTGGCGGCTTGTGAAAGAA 791
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QY 792 CCGGATTTGAGAGTGGCGGCTTGTGAGAGAGCAGTGTACAGAGCTTAAAAAGGGCAA 851
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Db 720 GAATCAGCAGCAAGCAAGCAAAATCCCGCAACAGCAGTGTACTTACTTACGCTGATGTT 779
QY 911 TGAATGTGAAGAAATACGGGCCCAAGTACTGCGGTTCC--TCCGTGAGAGCGCCATGCT 967
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QY 968 GCACGCCCCAGCTGACAGAGACTGTGAGA 997
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LOCUS B0222696
DEFINITION AGENOUT_7546349 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:6025148
5', mRNA sequence.
ACCESSION B0222696
VERSION B0222696.1 GI:20404096
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

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REFERENCE NIH-MGC http://mgi.ncl.nih.gov/
AUTHORS 1 (bases 1 to 866)
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: AFCC
cDNA Library Preparation: Life Technologies, Inc.

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FEATURES
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    /issue_type="epithelioid carcinoma"
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    /note="Organ: pancreas; Vector: pCMV-Sport6; Site:1; NotI;
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    Technologies."
BASE COUNT 222 a 230 c 240 g 174 t
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Query Match 69 6%; Score 797.6; DB 14; Length 866.
Best Local Similarity 98.8%; Pred. No. 2.1e-210;
Matches 846; Conservative 0; Mismatches 4; Indels 6; Gaps 4:
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QY 245 CCAGCTCCACCGCTGTGAAGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCTGTGAAT 304
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QY 305 ATTAAGTCCGAATCTCCAAAAGGGGAAAGTTTCCAGGCCCAAGTGTAAACATCAGTGA 364
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Db 122 ATTAAGTCCGAATCTCCAAAAGGGGAAAGTTTCCAGGCCCAAGTGTAAACATCAGTGA 181
QY 365 CATGTAATGATGGCGCGTGGCTGCATTCCTGTGTCTCCCAAGAACTATCTCTCCCA 424
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QY 425 ACTTGGGCTGTCCCAACCTCGGCTGTGTAAAGTTACCGGGCAGTCTCGAGAGTGGG 484
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QY 485 TCTGTACAGAGATAGTATCAAGAGACCCCATGAGAGACAGAGGCGCTCTTGGCAAG 544
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Db 302 TCTGTACAGAGATAGTATCAAGAGACCCCATGAGAGACAGAGGCGCTCTTGGCAAG 361
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QY 725 CCTGTGAGAACTGTATCTCCACAGAGTTACCAATGACAAACCTGAGTCCGCTTGTGA 784
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QY 785 AAGAAACCGGATTTGTAGGTGCGGCTTGTGAGACAGCAGTATGACAGCAGCAGAA 844
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 QY 964 TGTGTCACGCGCCCGCTGACCGAGCTGTGAAATG-CGGTTCGGTGGCAAGAT-6GGG 1021
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 DEFINITION AGENCOURT_8207494 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6283134
 5', mRNA sequence.
 ACCESSION B0644239
 VERSION B0644239.1 GI:21768411
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE NIH-MGC http://mgc.ncl.nih.gov/
 1 (bases 1 to 939)
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: rgs@bhs-remail.nih.gov
 Tissue Procurement: CGAP (Stanford)
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
 DNA sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LIML at:
 http://image.llnl.gov
 Plate: LCM2478 row: k column: 07
 High quality sequence stop: 637.
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 /clone="IMAGE:6283134"
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 /tissue_type="hepatocellular carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: liver; Vector: pOTB7; Site:1: XhoI; Site:2:
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 GGCACGAG(6). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-CDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH-MGC
 Library."
 BASE COUNT 248 a 249 c 247 g 195 t
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 Query Match 67.2%; Score 769.6; DB 14; Length 939;
 Best Local Similarity 94.6%; Pred. No. 1.3e-202;
 Matches 808; Conservative 0; Mismatches 44; Indels 2; Gaps 1;
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 QY 276 AGCTCAGTCAGAGGCGCAGACCTCTGTAATTAACCTCAGATCTACCAAAAGGGGGAAG 335
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 DB 61 AGCTCAGTCAGAGGCGCAGACCTCTGTAATTAACCTCAGATCTACCAAAAGGGGGAAG 120

QY 336 TTTCACGCCCACTGTAAACATGATGTCACATGATATTGATGGCGCTGGCTGCATTC 395
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 DB 121 TTTCACGCCCACTGTAAACATGATGTCACATGATATTGATGGCGCTGGCTGCATTC 180
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 DB 181 TCTGTGTCCCAAGAACTATCTCTCCCAACTTGGGCTGTCCCAACCTTGGCTGTCAA 240
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 DB 241 AGTTACGGGCGAGCTGCGAGAGAGTGGGCTGTGAGAGATATGATCAAGAACCCCAT 300
 QY 516 GGAAGACACAGAGCGGCTCTCTTGGCAAGAGAGTGTGATGCTCCAGGTGAGATT 575
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 DB 301 GGAAGACACAGAGCGGCTCTCTTGGCAAGAGAGTGTGATGCTCCAGGTGAGATT 360
 QY 576 GAGGAGAAACATGATTTGATTTGAGTTGGAAGAAAGCAGCTCAGTGAAGCGCTCCTGT 635
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 QY 756 CAATGACACCCCTGATGTCGCCCTTTGGAAGAAACCAGATTTGTGAGGTGCGGCTTG 815
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 QY 936 GTACTGGGTTCTGCGGTGAGCGGCGAGTGTGACGCCCCAGCTGACAGAGACTGTGA 995
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 DB 719 GTACTGGGTTCTGCGGTGAGCGGCGAGTGTGACGCCCCAGCTGACAGAGACTGTGA 778
 QY 996 GATCGGTTCTGCGGTGAGCGGCGAGTGTGACGCCCCAGCTGACAGAGACTGTGA 1055
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 ACCESSION AL550072
 VERSION AL550072.1 GI:12886679
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 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 985)
 AUTHORS Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

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		/tissue.type="Placenta"
		/note="Vector: pcMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Peng Liang Life Technologies a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : filangli@life.com URL : http://fulllength.invitrogen.com "
BASE COUNT	197 a	333 c 266 g 179 t 10 others
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Query Match	66.5%	Score 762.4; DB 9; Length 985;
Best Local Similarity	98.8%	Pred. No. 1.4e-200;
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Oy	61	CTGGCGCTCTCCACCTGCGCCGCTGCTGCCACTGCCCCCTGGAGCGCCCAAGTGCGG 120
Db	267	CTGGCGCTCTCCACCTGCGCCGCTGCTGCCACTGCCCCCTGGAGCGCCCAAGTGCGG 326
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Oy	181	AACGAGAGCTCAGAGAAAACGACGCCCTGCGACACACACCAAGGGCTGGAAATGCAACTTC 240
Db	387	AACGAGAGCTCAGAGAAAACGACGCCCTGCGACACACCAAGGGCTGGAAATGCAACTTC 446
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Db	447	GCGCGCAGCTCCACCGCTCTGAAGGGAGTTGACAGAGTCACTCAGAGGGGACGACCTGT 505
Oy	301	GAAATTAATCTCAGAAATCTACCAAAAGGGGAAAGTTTCCAGCCCACTGTAAACATCAG 360
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Oy	361	TGCACATGTATTGATGGGCGGTGGGGTGGCAATCTCTGCTGTCGCCCAAGAAATATCTGTC 420
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Oy	421	CCCAACTTGGGCTGTCCCAACCTTGGGCTGGTCAAGAGTTACCGGGCAGTGTGCGCAGAG 480
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Db	806	GTTGGAAAAGGACAGCTCACTGAAGGCGCTCCCTGTTTTTGGAAATGAGAGCTGCAATCTCA 865
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ACCESSION	B0716204		
VERSION	B0716204.1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 876)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Dr. James R. Lupski cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: L14M13587 row: P column: 11 High quality sequence stop: 663. Location/Qualifiers 1. 876 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:6189946" /clone_lib="Lupski-sympathetic_trunk" /sex="male" /tissue_type="sympathetic trunk" /dev_stage="adult, 16 yr" /lab_host="DH10B" /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1: NotI; Site_2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCTCCAGCGGCTCG-3' and 5'-GACTAGCTTGTAGATCGCAGCGCGCCCTT(15)-3'. Size selected > 1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life Technologies."		
FEATURES			
SOURCE			
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Matches 805; Conservative	0; Mismatches 8; Indels 4; Gaps 4;		
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111			
Db	1 TCTTTGCAGCTCAGTCAGAGGGGAGACCTGTGAATATTAACCTCCAGATCTACCAAAACG	60	
329	GGGAAGTTTCCAGCCCAACTGTAAACATCATAGTCACATGTATTGATGGCCCGTGGCT	388	
111			
Db	61 GGGAAAGTTTCCAGCCCAACTGTAAACATCATAGTCACATGTATTGATGGCCCGTGGCT	120	
389	GCATTTCCTCTGTGTGCCAAGAGACTATCTCTCCCAACTTGGGCTGTGCCAACCTCGGC	448	
111			
Db	121 GCATTTCCTCTGTGTGCCAAGAGACTATCTCTCCCAACTTGGGCTGTGCCAACCTCGGC	180	
449	TGTCCTCAAGTTACCGGGGAGAGTCGTGGCGAGAGAGTGGGCTGTGAGAGAGATGTATCAAG	508	
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 Db 301 TGGAGTGCAGAGAAACAATGATGATTGCTGAGTTGGAAGGACGCTCACTGAAGCGGC 360
 QY 629 TCCCTGTTTGGAGTGAAGCTCCGATCTTATACACCCCTTTACAGGCCAGAAATGTA 688
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 QY 689 TTGTCACAAACACTCATGCTCCGAGTCCGATCAAGACCTGGAGTGTATCTCCACAC 748
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 Db 421 TTGTCACAAACACTCATGCTCCGAGTCCGATCAAGACCTGGAGTGTATCTCCACAC 480
 QY 749 GAGTTACCAATGACAAACCTGAGTCCGCTCTTGGAAAGAAACCCGATTTGTGAGTGC 808
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 Db 481 GAGTTACCAATGACAAACCTGAGTCCGCTCTTGGAAAGAAACCCGATTTGTGAGTGC 540
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 QY 989 CTGTG-AAAGATCCGCTCCGCTGCGAAGAT-86GAGACATTTTCCAGAACGTAT-CA 1045
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 ACCESSION B0644666
 VERSION B0644666.1 GI:21768838
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 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 992)
 AUTHORS NIH-MGC <http://mgi.nhl.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: CGAP (Stanford)
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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 /note="Organ: liver; Vector: pOTB1; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACAGC(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the Laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library."
 BASE COUNT 268 a 257 c 258 g 208 t 1 others
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 Query Match 65.6%; Score 751.6; DB 14; Length 992;
 Best Local Similarity 98.1%; Pred. 1.4e-197;
 Matches 760; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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 Db 25 CCAACCAAGGGGCTGGAAATGCAACTTGGGCGCCAGCTCCACCGCTGAGGGATCTGC 84
 QY 274 AGAGCTCATGACAGAGGCGAAGCCCTGTAATTAATCTCCAGATCTACCAAAAGGGGAA 333
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 Db 85 AGAGCTCATGACAGAGGCGAAGCCCTGTAATTAATCTCCAGATCTACCAAAAGGGGAA 144
 QY 334 AGTTCCAGCCCACTGAATCAATGATGATGATGATGATGATGATGATGATGATGATGAT 393
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 Db 145 AGTTCCAGCCCACTGAATCAATGATGATGATGATGATGATGATGATGATGATGATGAT 204
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 Db 205 CCTCTGTGCTCCCAAGAACTATCTCTCCCAACTTGGGCTGTCCCAACCTCGCTGCTC 264
 QY 454 AAAGTTACCGGCGAGTGTGCGAGAGAGTGGGCTGTGACGAGATGATGATGATGATGATGAT 513
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 Db 265 AAAGTTACCGGCGAGTGTGCGAGAGAGTGGGCTGTGACGAGATGATGATGATGATGATGAT 324
 QY 514 ATGAGAGCAGAGAGCGGCTCTCTTGGCAAGAGAGTGGGATTCGATGCTCGAGGCTGAG 573
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 Db 325 ATGAGAGCAGAGAGCGGCTCTCTTGGCAAGAGAGTGGGATTCGATGCTCGAGGCTGAG 384
 QY 574 TTGACGAGAAACATGATTTGATTCAGTTGGAAAGGACGCTCACTGAAGCGGCTCCT 633
 |||||||
 Db 385 TTGACGAGAAACATGATTTGATTCAGTTGGAAAGGACGCTCACTGAAGCGGCTCCT 444
 QY 634 GTTTTGGAGATGAGACCTCGCATCTCTATACAAACCTTTACAAAGCCAGAAATGATGAT 693
 |||||||
 Db 445 GTTTTGGAGATGAGACCTCGCATCTCTATACAAACCTTTACAAAGCCAGAAATGATGAT 504
 QY 694 CAACCAACTTCAATGCTCCAGTGTCAAAAGACCTGTGAACCTGTATCTCCACAGAGTT 753
 |||||||
 Db 505 CAACCAACTTCAATGCTCCAGTGTCAAAAGACCTGTGAACCTGTATCTCCACAGAGTT 564
 QY 754 ACCAATGACAAACCTGAGTGTGCGGCTGTGAAAGAAACCCGGATTTGTAGGTGGGCT 813
 |||||||
 Db 565 ACCAATGACAAACCTGAGTGTGCGGCTGTGAAAGAAACCCGGATTTGTAGGTGGGCT 624
 QY 814 TGTGACAGCCAGTGTATACAGAGCTGAAAGGCAAGAAATGACAGAACCAAGAA 873
 |||||||
 Db 625 TGTGACAGCCAGTGTATACAGAGCTGAAAGGCAAGAAATGACAGAACCAAGAA 684
 QY 685 TCCCGGCAACAGTGTGAGTTTACCTGTGATGATGATGATGATGATGATGATGATGATGAT 744
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 Db 745 AAGTACTGCGGTTCTCTGCTGAGAGCGGATGCTGACGCCACCTGACCAAGCA 988
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 Db 988 AAGTACTGCGGTTCTCTGCTGAGAGCGGATGCTGACGCCACCTGACCAAGCA 799

[illegible]

Query Match	Best Local Similarity	55.3%	Score 748.8	DB: 9	Length 1009
Matches 766; Conservative	95.8%; Pred. No. 8.4e197;	20;	Mismatches 12;	Gaps 2;	Indels 2;

OY		4	AGCTCCCGCATTCGACGAGGGGCGCTGCCTTATGTGTCACACCCTTTCACACTTGACACAGGCTG	63
Db		212	AGCTCCCGCATTCGACGAGGGGCGCTGCCTTATGTGTCACACCCTTTCACACTTGACACAGGCTG	271
OY		64	GCGCTTCACACTGCCCCGGCTGCCTTGCCTACCTGCCCTTGGAGGGGCCCAAGTGGCGCG	123
Db		272	GCGCTTCACACTGCCCCGGCTGCCTTGCCTACCTGCCCTTGGAGGGGCCCAAGTGGCGCG	331
OY		124	GGAATGGGGCTGCTCCGGGACGGCTGGCGCTGCTGTAAAGTTCTGCGCCCAAGCAAGCTCAAC	183
Db		332	GGAATTAGGGCTGTGTCGCGGAMGGCTGCGGGCTGCTGTAAAGTTCTGCGCCCAAGCAAGCTCAAC	391
OY		184	GAGACATGCGCAAAAAGCAGGCCCTTGACACAACCAAAGGGGCGGAAATGCAATTCGGC	243
Db		392	GARAAATMGCAAAAAAGCAGGCCCTTGACACAACCAAAGGGGCGGAAATGCAATTCGGC	451
OY		244	GCCAGCTCCACCCGCTGGAAGGGGATGTGAGAAGCTAGTCAGAGGGGCAAGCCCTGTGAA	303
Db		452	GCCA -CACCAOCGCTTAAARGGATMTGCAACAGCTAGTMARAGGGCAACACTGTAA	510
OY		304	TATTAATCTCCAGATCTACCAAAAAGGGGAAAGTTTCCAGCCCAACTGTAAACATCACTAGTC	363
Db		511	TATTAATCTCCAGATCTACCAAAAAGGGGAAAGTTTCCAGCCCAACTGTAAACATCACTAGTC	570
OY		364	ACATGTTATGATGGGCGCGTGGGCTGATTCCTGTGTGCCAAGAACATATCTCTCCC	423
Db		571	ACATGTTATGATGGGCGCGTGGGCTGATTCCTGTGTGCCAAGAACATATCTCTCCC	630
OY		424	AACCTTGGGCTGTCCCAACCTCGCGCTGGTCAAAATTACGGGGAGTCTGTGAGAGATGG	483
Db		631	AACCTTGGGCTGTCCCAACCTCGCGCTGGTCAAAATTACGGGGAGTCTGTGAGAGATGG	690
OY		484	GTCGTGACGAGATAGTATCAAGAGCCCATGAGGAGGACCAAGCAGCAGGCTCTCTTGGCAAG	543
Db		691	GTCGTGACGAGATAGTATCAAGAGCCCATGAGGAGGACCAAGCAGCAGGCTCTCTTGGCAAG	750
OY		544	GAGCTGGGATTCGATGGCTCCGAGCTGGAGTGTACGAGAAACAATGAATTGATTCAGTT	603
Db		751	GAGCTGGGATTCGATGGCTCCGAGCTGGAGTGTACGAGAAACAATGAATTGATTCAGTT	810
OY		604	GGAATAAGCAGCTACTGAAAGCGGCTCCCTGTTTTTGGAAATGAGCCTCGCATCTTAC	663
Db		811	GGAATAAGCAGCTACTGAAAGCGGCTCCCTGTTTTTGGAAATGAGCCTCGCATCTTAC	870
OY		664	AACCTTTTACAGGSCGAAATGTATTGTTCACAAACAATTGATGTCGCCAGTGTCAAG	723
Db		871	AACCTTTTACAGGSCGAAATGTATTGTTCACAAACAATTGATGTCGCCAGTGTCAAG	930
OY		724	ACCTGTGGAACTGGTATCTCCACACGAGTTTACCAATGACAACCTTGAGTGGCGCTTGTG	783
Db		931	ACCTGTGG -AATGGTATCTCCACACGAGTTTACCAATGAMAACCTTGAGTGGCGCTTGTG	989
OY		784	AAAGAACCCCGATTGTGA	803
Db		990	AAAAAAAAACCCGATTGTGA	1009
RESULT 11				
BQ716992				
LOCUS				
DEFINITION			836 bp mRNA linear EST 16-JUL-2002	
IMAGE:6187193 5'			mRNA	
IMAGE:6187193 5'			lupsk1_sympathetic_trunk Homo sapiens cDNA clone	
ACCESSION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
Homo sapiens				
Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.				
1 (bases 1 to 836)				
NIH-MGC http://mgc.nci.nih.gov/.				
National Institutes of Health, Mammalian Gene Collection (MGC)				

JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov
Plate: LLM13580 row: m column: 18
High quality sequence stop: 731.

FEATURES

source

location/Qualifiers

1. 836

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6187193"
/clone_lib="Lupski_sympathetic_trunk"
/sex="male"
/tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6 (Life Technologies); site:1; NotI; site:2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCAGCGGCTCG-3' and 5'-GACTAGTTCTAGATCGGAGCGGCCGCTT(5')-3'. Size selected > 1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life Technologies."

BASE COUNT

215 a 221 c 235 g 165 t

ORIGIN

Query Match 65.1%; Score 746; DB 14; Length 836;
Best local similarity 99.9%; Pred. No. 4.5e-196;
Matches 757; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 139 CGGAGCGGCTCGGCTGCTGTAGGTGTGCCAAGCAAGCTCAACGAGAGCTGCAGCAA 198
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Db 1 CGGAGCGGCTCGGCTGCTGTAGGTGTGCCAAGCAAGCTCAACGAGAGCTGCAGCAA 60

QY 199 ACGAGCGCTTCGACACACACCAAGGGGTGTAATATGCAACTTGGCGCGCAGCTCCACCGCT 258
|||
Db 61 ACGAGCGCTTCGACACACCAAGGGGTGTAATATGCAACTTGGCGCGCAGCTCCACCGCT 120

QY 259 CTGAAGGGGATCTGAGAGCTCAATGCAAGGGGAGACCTGTGAATATTAATCCAGAAATC 318
|||
Db 121 CTGAAGGGGATCTGAGAGCTCAATGCAAGGGGAGACCTGTGAATATTAATCCAGAAATC 180

QY 319 TACCAAAAAGGGGAAAGTTTTCAGAGCCCAACTGTAAACATCAGTGCACATGTATTGATGGC 378
|||
Db 181 TACCAAAAAGGGGAAAGTTTTCAGAGCCCAACTGTAAACATCAGTGCACATGTATTGATGGC 240

QY 379 GCCGTGGGCTCATTTCTCTGTGTGCCAAGACTATCTTCGCCACTTGGCGCTGCC 438
|||
Db 241 GCCGTGGGCTCATTTCTCTGTGTGCCAAGACTATCTTCGCCACTTGGCGCTGCC 300

QY 439 AACCTCGGCTGATCAAGTTACGGGGGAGTGTCCGAGGAGTGGGGTGTGACAGGAGAT 498
|||
Db 301 AACCTCGGCTGATCAAGTTACGGGGGAGTGTCCGAGGAGTGGGGTGTGACAGGAGAT 360

QY 499 AGTATCAAGAGACCCCATGAGAGACAGACGCGCTCTTTGGCAAGAGAGCTGGATTCCAT 558
|||
Db 361 AGTATCAAGAGACCCCATGAGAGACAGACGCGCTCTTTGGCAAGAGAGCTGGATTCCAT 420

QY 559 GCCTCCGAGGTGGAGTTGACAGAGAAACATGAATTGATTTGAGTTGAAAAAGCAGCTCA 618
|||
Db 421 GCCTCCGAGGTGGAGTTGACAGAGAAACATGAATTGATTTGAGTTGAAAAAGCAGCTCA 480

QY 619 CTGAAGGGGCTCCCTGTTTGGGAATGAGGCTGCATCTATACACCCCTTTACAAAGC 678
|||

Db 481 CTGAGCGGCTCCCTGTTTGGATGAGACCTGCGATTCCTATACAACTTTACAAAGC 540
 QY 679 CAGAAATGATGTGTTCAACACACTGATGCTCCAGTGTCAAAAGACCTGTGAACTGT 738
 Db 541 CAGAAATGATGTGTTCAACACACTGATGCTCCAGTGTCAAAAGACCTGTGAACTGT 600
 QY 739 ATCTCCACAGAGTTACCAATGACAACTGAGTCCGCTGTGAAAGAACCCGGATT 798
 Db 601 ATCTCCACAGAGTTACCAATGACAACTGAGTCCGCTGTGAAAGAACCCGGATT 660
 QY 799 TGTGAGTGGGCTGTGTGAGACGCGATGTACAGCCTGGAAGGAGCAAGAAATGC 858
 Db 661 TGTGAGTGGGCTGTGTGAGACGCGATGTACAGCCTGGAAGGAGCAAGAAATGC 720
 QY 859 AGCAGACCAAGAAAT-CCCCCGACACGCTCAGGTTTA 895
 Db 721 AGCAGACCAAGAAATCCCCCGACACGCTCAGGTTTA 758

RESULT 12

BQ720988 908 bp mRNA linear EST 16-JUL-2002
 LOCUS AGENCOURT_B103841 lupski_sympathetic_trunk Homo sapiens cDNA clone
 DEFINITION IMAGE:6190963 5', mRNA sequence.

ACCESSION BQ720988
 VERSION BQ720988.1 GI:21859885
 KEYWORDS EST.

SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 908)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
 Plate: LLM13590 row: 3 column: 20
 High quality sequence stop: 582.

FEATURES

source
 1..908
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:6190963"
 /clone_lib="Lupski_sympathetic_trunk"
 /sex="male"
 /tissue_type="sympathetic trunk"
 /dev_stage="adult, 16 yr"
 /lab_host="DH10B"
 /note="Vector: PCMV-SPORT6 (Life Technologies); Site 1: NotI; Site 2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TGCAGCCAGCGCG-3' and 5'-GACTACTTCTACATGCGGAGGCGCCCT(15)-3'. Size selected > 1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life Technologies."
 BASE COUNT 237 a 224 c 246 g 200 t 1 others

Query Match 64.5%; Score 738.6; DB 14; Length 908;
 Best Local Similarity 98.7%; Pred. No. 5.4e-194;
 Matches 755; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY 383 TGGGCTGATTCCTCTGTGTCCCAAGAACTATCTCTCCCACTGGGCTGCCAAC 442
 Db 2 TGGGCTGATTCCTCTGTGTCCCAAGAACTATCTCTCCCACTGGGCTGCCAAC 61
 QY 443 CTCGGCTGCTCAAGTTACCGGGCAGTGTGCGAGAGTGGTGTGAGAGAGTA 502
 Db 62 CTCGGCTGCTCAAGTTACCGGGCAGTGTGCGAGAGTGGTGTGAGAGAGTA 121
 QY 503 TCAAGACCCCATGAGAGACAGAGCGGCTCTCTGGCAAGAGCTGGATTCCT 562
 Db 122 TCAAGACCCCATGAGAGACAGAGCGGCTCTCTGGCAAGAGCTGGATTCCT 181
 QY 563 CCGAGGTGAGTTGAGAGAGAAACATGATGATGATGATGATGATGATGATGAT 622
 Db 182 CCGAGGTGAGTTGAGAGAGAAACATGATGATGATGATGATGATGATGATGAT 241
 QY 623 AGGGGCTCCCTGTTTGGATGAGAGCTGCTGATTCATCAACCTTTTCAAGGCG 682
 Db 242 AGGGGCTCCCTGTTTGGATGAGAGCTGCTGATTCATCAACCTTTTCAAGGCG 301
 QY 683 AATGATGTTTCAACAACTTCATGCTCCAGTGTCAAGAGCTGTGAACTGATCT 742
 Db 302 AATGATGTTTCAACAACTTCATGCTCCAGTGTCAAGAGCTGTGAACTGATCT 361
 QY 743 CCACAGAGTTACCAATGACAACTGAGTGGCGCTTGTGAAGAAACCCGATTTG 802
 Db 362 CCACAGAGTTACCAATGACAACTGAGTGGCGCTTGTGAAGAAACCCGATTTG 421
 QY 803 AGGTGGGCTGTTTGGAGAGCCAGTGTACAGAGCTGTGAAGAGGCAAGATGACGA 862
 Db 422 AGGTGGGCTGTTTGGAGAGCCAGTGTACAGAGCTGTGAAGAGGCAAGATGACGA 481
 QY 863 AGACCAAGAAATCCCCGAAACAGTCAAGTGTACTTACGCTGATTTTGAAGTGA 922
 Db 482 AGACCAAGAAATCCCCGAAACAGTCAAGTGTACTTACGCTGATTTTGAAGTGA 541
 QY 923 AATACCGGCGCAAGTACTGCGGTTCTGCGTGGAGCGCGATGCTGACGCGCTGA 982
 Db 542 AATACCGGCGCAAGTACTGCGGTTCTGCGTGGAGCGCGATGCTGACGCGCTGA 601
 QY 983 CCAGGACTGTGAAGATGCGGTTCCGCTGGAGAGATGGG-GAGCATTTTCCAGAACGTC 1041
 Db 602 CCAGGACTGTGAAGATGCGGTTCCGCTGGAGAGATGGG-GAGCATTTTCCAGAACGTC 661
 QY 1042 ATGATGATCAGAGCTGTCAAAATGCACTCACTACGCGCCGATCCCAATGAAGCGGTT 1101
 Db 662 ATGATGATCAGAGCTGTCAAAATGCACTCACTACGCGCCGATCCCAATGAAGCGGTT 721
 QY 1102 CCTTTTACAGGCTGTTCAATGACATTCACAAATTTAGGACTTA 1146
 Db 722 CCTTTTACAGGCTGTTCAATGACATTCACAAATTTAGGACTTA 766

RESULT 13

BQ719732 896 bp mRNA linear EST 16-JUL-2002
 LOCUS AGENCOURT_B305072 lupski_sympathetic_trunk Homo sapiens cDNA clone
 DEFINITION IMAGE:6193402 5', mRNA sequence.

ACCESSION BQ719732
 VERSION BQ719732.1 GI:21858629
 KEYWORDS EST.

SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 896)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 cDNA Library Preparation: Life Technologies, Inc.

Query Match 64.5%; Score 738.6; DB 14; Length 908;
 Best Local Similarity 98.7%; Pred. No. 5.4e-194;
 Matches 755; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: LLM13596 row: P column: 11
 High quality sequence stop: 577.

FEATURES

source

1. 896

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_image="IMAGE:6193402"

/clone_id="Lupski_sympathetic_trunk"

/sex="male"

/tissue_type="sympathetic trunk"

/dev_stage="adult, 16 yr"

/lab_host="DH10B"

/note="Vector: pCMV-SPORT6 (Life Technologies); site_1:
 NotI; site_2: SalI; cDNA made by oligo-dT priming.
 Directionally cloned using the following adaptors:
 5'-TCGACCCAGCGTCG-3' and
 5'-GACTAGCTTACAGTACGAGCGGCCCT(15)-3'. Size selected >
 1 kb for average insert length 1.9 kb. This is a primary
 library, non-amplified. Library constructed by Life
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
 College of Medicine); available through Life
 Technologies."

BASE COUNT 203 a 275 c 249 g 169 t
 ORIGIN

Query Match

Best Local Similarity 63.4%; Score 726; DB 14; Length 896;
 Matches 796; Conservative 0; Mismatches 25; Indels 5; Gaps 5;

QY 1 ATGAGCTCCCGATCGCCAGGCGCTGCTTACTGTCACCTTCTCCACTTGACCAAG 60
 DB 45 ATGAGCTCCCGATCGCCAGGCGCTGCTTACTGTCACCTTCTCCACTTGACCAAG 104
 QY 61 CTGGCGCTCTCCACCTGCGCGCTGCTGCGACCTGCGCGCGCGCGCGCGCGCGCG 120
 DB 105 CTGGCGCTCTCCACCTGCGCGCTGCTGCGACCTGCGCGCGCGCGCGCGCGCGCG 164
 QY 121 CCGGAGCTGGGCTGTCGCGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
 DB 165 CCGGAGCTGGGCTGTCGCGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 224
 QY 181 AAGCAGCTGCGACAAACGACGCGCTGCGACCAACCAAGGCGCTGGAATGCACTTC 240
 DB 225 AAGCAGCTGCGACAAACGACGCGCTGCGACCAACCAAGGCGCTGGAATGCACTTC 284
 QY 241 GCGGCGCTGCGACCGCTGGAAGGGGATGTCGACAGCTCACTGAGAGGCGACCGCT 300
 DB 285 GCGGCGCTGCGACCGCTGGAAGGGGATGTCGACAGCTCACTGAGAGGCGACCGCT 344
 QY 301 GAATATTAATCCAGAAATCTACCAAAAGGGGAAAGTTCCAGCCCACTGTAACATCAG 360
 DB 345 GAATATTAATCCAGAAATCTACCAAAAGGGGAAAGTTCCAGCCCACTGTAACATCAG 404
 QY 361 TGCACATGATATGATGCGCGCGCTGCGATTCCTCTGTCGCCCAAGAACTATCTC 420
 DB 405 TGCACATGATATGATGCGCGCGCTGCGATTCCTCTGTCGCCCAAGAACTATCTC 464
 QY 421 CCCAACTTGGGCTTCCCAACCCCTGGCTGCTCAAAATTCAGGGGAGTGTGAGAGAG 480
 DB 465 CCCAACTTGGGCTTCCCAACCCCTGGCTGCTCAAAATTCAGGGGAGTGTGAGAGAG 524
 QY 481 TGGGCTGTGACGAGATATATCAAGACCCCATGAGAGACGAGAGCGGCTCTTGGC 540
 DB 525 TGGGCTGTGACGAGATATATCAAGACCCCATGAGAGACGAGAGCGGCTCTTGGC 584
 QY 541 AAGAGCTGGGATTCGATGCTT -CCGAGGTGAGATTCAGCAAGAAACATGATGATTC 599
 DB 585 AAGAGCTGGGATTCGATGCTTCCCGAAGTGGAGTTGACGAGAAACATGATGATTC 644

QY 600 AGTTGAAAAGGACGCTCACTGAGAGCGGCTCCCT -GTTTGGATGAGCTTCGATCC 658
 DB 645 AGTTGAAAAGGACGCTCACTGAGAGCGGCTCCCTGTTTGGATGAGAGCTTCGATCC 704
 QY 659 TATACAACTTACAGAGCGCAGAAATGATTTGTCACCACTTACAGTGTCCAGTGC 718
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 QY 719 CAAGACCTGTG -AACTGATTCACACAGAG -TTACCAATGACACCTGATGCCG 776
 DB 765 CAAGACCTGTGAGAGAGGATATCTCCCCGAGTTTACCATTCGAAACCTGATGCC 824
 QY 777 CCTTGTGAAAGAAA -CCCGATTTGTGAGGTCGCGCTTGTGACA 821
 DB 825 CCCTGTGAAAGAAAACCCGAGATTTGGAGTGCAGGCTTGGGCA 870

RESULT 14

AL541592

LOCUS

AL541592 LTL_FL002_P11 Homo sapiens cDNA clone CS0DE003YE20 5 prime

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

location/Qualifiers

1. 929

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_image="CS0DE003YE20"

/clone_id="LTL_FL002_P11"

/lab_host="DH10B"

/note="Organ: Placenta; Vector: pCMVSPORT 6; 1st strand
 cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-stranded cDNA was digested with Not I
 and cloned into the Not I and Eco RV sites of the
 pCMVSPORT 6 vector. Library was constructed by Life
 Technologies. Contact: Feng Liang Life Technologies, a
 division of Invitrogen 9800 Medical Center Drive Rockville
 , Maryland 20850, USA fax: (1) 301 610 8371 Email:
 fliang@lifestech.com URL:
<http://fulllength.invitrogen.com>"

BASE COUNT 182 a 323 c 257 g 166 t 1 others
 ORIGIN

Query Match

Best Local Similarity 63.1%; Score 722.6; DB 9; Length 929;
 Matches 722; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCTCCCGATCGCCAGGCGCTGCTTACTGTCACCTTCTCCACTTGACCAAG 60
 DB 207 ATGAGCTCCCGATCGCCAGGCGCTGCTTACTGTCACCTTCTCCACTTGACCAAG 266
 QY 61 CTGGCGCTCTCCACCTGCGCGCTGCTGCGACCTGCGCGCGCGCGCGCGCGCGCG 120
 DB 267 CTGGCGCTCTCCACCTGCGCGCTGCTGCGACCTGCGCGCGCGCGCGCGCGCGCG 326
 QY 121 CCGGAGCTGGGCTGTCGCGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
 DB 327 CCGGAGCTGGGCTGTCGCGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 386

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QY 181 AACGAGACTGCAGCAAAACGACGCCCTGGACACACAGGGGCTGGAATGCAACTTC 240
DB 387 AACGAGACTGCAGCAAAACGACGCCCTGGACACACAGGGGCTGGAATGCAACTTC 446
QY 241 GGGGCCAGCTCCACCCCTCTGAAAGGGGATCTGCAGAGCTCAGTCAAGAGGACACCTGT 300
DB 447 GGGGCCAGCTCCACCCCTCTGAAAGGGGATCTGCAGAGCTCAGTCAAGAGGACACCTGT 506
QY 301 GAATATACCTCCAGATCTACCAAAACGGGGAAAGTTTCCAGCCCACTGTAACATCAG 360
DB 507 GATATATACCTCCAGATCTACCAAAACGGGGAAAGTTTCCAGCCCACTGTAACATCAG 566
QY 361 TGCACATGTATGATGGCCCGCTGGCTGCATCTCTGTCTCCCAAGAACTATCTCTC 420
DB 567 TGCACATGTATGATGGCCCGCTGGCTGCATCTCTGTCTCCCAAGAACTATCTCTC 626
QY 421 CCCAACTGGGGCTGCTCCCAACCCCTGGCTGGTCAAGTTACCGGGAGTGGTCCGAGAG 480
DB 627 CCCAACTGGGGCTGCTCCCAACCCCTGGCTGGTCAAGTTACCGGGAGTGGTCCGAGAG 686
QY 481 TGGGCTGTGACGAGAGATAGTATCAAGACCCCATGGAGACCGAGCCCTCTTGGC 540
DB 687 TGGGCTGTGACGAGAGATAGTATCAAGACCCCATGGAGACCGAGCCCTCTTGGC 746
QY 541 AAGGACCTGGGATTCGATGCTCTCCGAGTGGAGTTGACGAGAAACAATGATGATGCA 600
DB 747 AAGGACCTGGGATTCGATGCTCTCCGAGTGGAGTTGACGAGAAACAATGATGATGCA 806
QY 601 GTTGGAAAAGGACGCTACGTAAGCGGCTCCCTGTTTGGAAATGAGAGCTGCATCTCA 660
DB 807 GTTGGAAAAGGACGCTACGTAAGCGGCTCCCTGTTTGGAAATGAGAGCTGCATCTCA 866
QY 661 TACAACCTTTTACAAGGCGCAAAATGATTTTCAACAACATCATGTCCTCCAGTCTCA 720
DB 867 TACAACCTTTTACAAGGCGCAAAATGATTTTCAACAACATCATGTCCTCCAGTCTCA 926
QY 721 AAG 723
DB 927 AAG 929

RESULT 15
LOCUS BM479014 1083 bp mRNA linear EST 05-FEB-2002
DEFINITION AGENCOUT_6466996 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5561420
ACCESSION BM479014
VERSION 5', mRNA sequence.
KEYWORDS EST.
SOURCE EST.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1083)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL2289 row: C column: 21
High quality sequence stop: 596.
Location/Qualifiers
1..1083
/organism="Homo sapiens"
/db_xref="taxon:9606"

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/clone="IMAGE:5561420"
/issue_lib="NIH_MGC_88"
/issue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: small intestine; Vector: pCMV-Sport6;
Site_1: NotI; Site_2: SalI; Cloned unidirectionally;
oligo-dr primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH-MGC Library."
BASE COUNT 275 a 314 c 242 g 252 t
ORIGIN
Query Match 62.3%; Score 714; DB 13; Length 1083;
Best Local Similarity 96.3%; Pred. No. 4.1e-187;
Matches 763; Conservative 0; Mismatches 25; Indels 4; Gaps 3;
QY 243 CGCAGCTCCACCGCTCTGAGGGGATCTGCAGAGCTCAGTCAAGAGGACGACCCCTGTA 302
DB 1 CGCAGCTCCACCGCTCTGAGGGGATCTGCAGAGCTCAGTCAAGAGGACGACCCCTGTA 60
QY 303 ATATTAATCCAGATCTACCAAAACGGGGAAAGTTTCCAGCCCACTGTAACATCAGT 362
DB 61 ATATTAATCCAGATCTACCAAAACGGGGAAAGTTTCCAGCCCACTGTAACATCAGT 120
QY 363 CACATGTATGATGGCCCGCTGGCTGCATCTCTGTCTCCCAAGAACTATCTCTCC 422
DB 121 CACATGTATGATGGCCCGCTGGCTGCATCTCTGTCTCCCAAGAACTATCTCTCC 180
QY 423 CAACCTGGGGCTGCCCAACCCCTGGCTGCAAGTTACCGGGAGTGGTGGAGAGT 482
DB 181 CAACCTGGGGCTGCCCAACCCCTGGCTGCAAGTTACCGGGAGTGGTGGAGAGT 240
QY 483 GGTCTGTGACGAGATAGTATCAAGAGCCCATGAGAGACGAGGCTCTTGGCA 542
DB 241 GGTCTGTGACGAGATAGTATCAAGAGCCCATGAGAGACGAGGCTCTTGGCA 300
QY 543 GAGCTGGGATTCGATGCTCCGAGGTGAGATTGACGAGAAACAATGATGATGAT 602
DB 301 GAGCTGGGATTCGATGCTCCGAGGTGAGATTGACGAGAAACAATGATGATGAT 360
QY 603 TGGAAAAGGACGCTACGTAAGCGGCTCCCTGTTTGGAAATGAGAGCTGCATCTCA 662
DB 361 TGGAAAAGGACGCTACGTAAGCGGCTCCCTGTTTGGAAATGAGAGCTGCATCTCA 420
QY 663 CAACCTTTACAAGGCGCAAAATGATTTTCAACAACATCATGTCCTCCAGTCTCA 722
DB 421 CAACCTTTACAAGGCGCAAAATGATTTTCAACAACATCATGTCCTCCAGTCTCA 480
QY 723 GACCTGTGAACTGTATCTCCACAGAGTACCAATGACAACCCCTGATGGCCCTGT 782
DB 481 GACCTGTGAACTGTATCTCCACAGAGTACCAATGACAACCCCTGATGGCCCTGT 540
QY 783 GAAAGAAACCCGATTTTGAAGTGGCGGCTGTGACAGCCAGTGTACAGAGCTGAA 842
DB 541 GAAAGAAACCCGATTTTGAAGTGGCGGCTGTGACAGCCAGTGTACAGAGCTGAA 600
QY 843 AAAGGGCAAGAAATGACAGCAAGCAAGAAAT-CCCGGAAACAGTCAAGTTTACTTAC 901
DB 601 AAAGGGCAAGAAATGACAGCAAGCAAGAAATCCCGGAAACAGTCAAGTTTACTTAC 660
QY 902 CTGAGATTTGAGTGTGAAGAAATACCGCCCAAGTACGCGGTTCC--TGGTGGAGG 959
DB 661 CTGAGATTTGAGTGTGAAGAAATACCGCCCAAGTACGCGGTTCC--TGGTGGAGG 720
QY 960 CCGATGCTCAGCGCCCACTGACAGAGACTGTG-AGATGGGTTTCCGCTCGAAGATG 1018
DB 721 CCGATGCTCAGCGCCCACTGACAGAGAGTGAAGATGCCGTTCCCTTCGAAAAA 780
QY 1019 GGGAGACATTTT 1030
DB 781 TGGGGAACATTT 792

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Fri, Jul 11 08:51:01 2003

Search completed: July 10, 2003, 09:52:16
Job time : 1915 secs

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